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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/ptTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ptTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 4, Appli Sequence 169999, Sequence 17003, Sequence 17000, Sequence 17000, Sequence 170000, Sequence 170000, Sequence 1670, A Sequence 167034, Sequence 1543, A Sequence 1554, A Sequence 1554, A Sequence 1554, A Sequence 1554, A Sequence 1554, A Sequence 1559, A Sequence 1278, Ap Sequence 1278, Ap Sequence 1278, Ap	Proteins and Polynucleotides l	Length 2736;       Indels
3 US-09-306-902A-4 4 US-09-949-016-169999 4 US-09-949-016-170033 4 US-09-471-276-345 4 US-09-949-016-170040 4 US-09-949-016-170040 4 US-09-949-016-170040 4 US-09-949-016-170003 4 US-09-571-479C-5 1 US-08-232-463-14 4 US-09-949-016-15544 4 US-09-949-016-15544 4 US-09-949-016-15544 4 US-09-949-016-15544 6 US-09-949-016-15544 8 US-09-970-767-158 8 US-09-270-767-16560 1 US-08-232-463-14	RESULT 1 US-09-969-532-9 Sequence 9, Application US/09969532 Patent No. 6777232 GENERAL INPORMATION: APPLICANT: Walke, D. Wade APPLICANT: Scoville, John TITLE OF INVENTION: No. 6777232el Human Membrane Prot TITLE OF INVENTION: NUMBER: US/09/969,532 CURRENT FILING DATE: 2001-10-02 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 33 NUMBER OF SEQ ID NOS: 33 LENGTH: 2736 TYPE: DAA TYPE: DAA TYPE: DAA TYPE: DAA US-09-969-532-9	04; Score 2736; DB 4; 0, Mismatches 0; 0; Mismatches 0; 0; Mismatches 0; GCCACCGCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
69.6 2.5 305 62.6 2.3 601 57 2.1 601 50.2 1.8 601 49.6 1.8 601 47 1.7 19326 42.4 1.5 4528 42.2 1.5 7218 42.2 1.5 75929 39.8 1.5 75929 39.6 1.4 1507 39 1.4 1507 37.8 1.4 1507	ULT 1 09-969-532-9 equence 9, Application US, atent No. 6777232 APPLICANT: Walke, D. Wade APPLICANT: Walke, D. Wade APPLICANT: Scoville, Joh FILE REFERENCE: LEX-0244-1CURRENT APPLICATION NUMBER: PRIOR PILING DATE: 2000-12000 PRIOR FILING PRIOR FILI	100   Best Local Similarity   100   Matches 2736; Conservative   1 ATGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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Pred. No. 0;
0; Mismatches
                   4.0
                   Version
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Best Local Similarity 97.3%;
Matches 2661; Conservative
  NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows
SEQ ID NO 15
                                                         TYPE: DNA
ORGANISM: homo sapiens
US-09-969-532-15
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Sequence 15, Application US/09969532

Patent No. 6777232

GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin'
TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin'
CURRENT ELENGTION NUMBER: US/09/969,532

CURRENT PILING DATE: 2001-10-02

PRIOR FILING DATE: 2000-10-02
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                                                                                                                  TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA
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Best Local Similarity   100.0%;   Pred. No. 0;   Matches 2043;   Conservative   0;   Mismatches 0;   Indels   0;   Gaps   0;	874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAACCTCTTCAT 9  181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 2  934 GAAATAAAACCCCAAAGCATTGAAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 9	241 GAMATAAAACCCCAAAGCATTGAGAATGCCAAGGACATTGCTTTGTACTCGGGGCTTGGGT 30 994 GCTGCCGTCGTGCCGTTGCAGTCCTGGTCATTGGTGTCTCAGACGAGGCAG 10 994 GCTGCCGTCGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGAGCCAG 10 301 GCTGCCGTCGCTGCAGTTGCAGTCCTCGTCATTGATCATCACCTTTACAGACGAGCCAG 36 1054 AGTGACTATGGCGTGGACGTCATTGACTTTTCAGATGTGACGTCTTCAGACGTGCAGTCTTCTCAGACTTCTTACAGACGTGGACCTTC 11	DD 351 AGIGACIAIGGCGIGGACGICATIGACICTICIGCATIGACAGGIGGCTICCAGACCTIC 420  QY 1114 AACTICAAAACAGICGGCAAGAATAICATGCAACGAACTAATGATACAAGAAAATC 1173  DD 421 AACTICAAAACAGICCGTCAAGCCAAGAATAICATGGAACTAATGATACAAGAAAATC 480  QY 1174 ȚITGGIAACȚCCCȚGCTCCAGACTGAGCCAGATCTGACAGAGAACAA 1233	UDb   1234 TTTGGTAACTCCCTGAATTCTGCAGCCAGATCTGCAGATCGAGATCGAGATCTGCAGATCAGAGAGCCGGACA 540	1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG	661 GGAGTGTCTGAGAGAGTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 7  1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1  721 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1	Qy         1474 TCATCACTCCCCACAAGGACAGAACTGAGTGACTGGTGTCTTTGGCCATTTAGGGGGG         1533           Db         781 TCATCACTCCCCAAAGGACAGAACTGAGGACAACTGGTGTTTTGGCGGG         840           Qy         1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGCGTCCCAGAG         1593		Dy         1654 GGCTCTGAGGTGCTCTGAAGTCTGAGTCACCTGTGGTCCTCCAGACATGATCGTCACC         1713           Db         961 GGCTCTGAGGTGCTCCTGAGTCCTCAGACTCTCCAGACATGATCGTCACC         1020	OY 1714 ACTCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773

Sequence 27, Application US/09969532 Patent No. 6777232 GENERAL, INFORMATION:	g &	688 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 747
APPLICANT: Walke, D. Wade APPLICANT: Scoville, John TITLE OF INVENTION: No. 677232el Human Membrane Proteins and Polymucleotides Encodin	g 9	
(969,532	P &	1534 GCTTAGTAATGCCAAATACAGGGTGAGCTTACTCATACCACAGGGGCCATCCCAGAG 1593 
PRIOR APPLICATION NUMBER: US 60/237,280 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0	දු අ	1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653 
; SEN ID NO 2/ ; LENGTH: 2010 ; TYPE: DNA ; ORGANISM: homo sapiens	Qy Dp	1654 GGCTCTGAGGTGCTCCTGAGTCCTGAGGTCCTCCTGGAGACATGATGGTCGTCGC 1713 
Ouery Match 71.9%; Score 1967; DB 4; Length 2010; Best Local Similarity 98.4%; Pred. No. 0;	රු අ	1714 ACTCCCTTTGCATTGACCATCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
Matches 2010; Conservative 0; Mismatches 0; Indels 33; Gaps 694 ATGGCAGCCAACATGTGGCAAGGAGGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG	oy da	1774 CATTTAAAGAAGACACAGCAGGGCAAATGGGAGGAAGTGATGTGAGGGAGG
OD 1 AIGSCRACCHACATCHICGIGGCIAAGAAGACCTGICGGCCACIGIIGIGGICIACGIG 80  QY 754 GAIGGGAGGAAGIGIGGAGGAATGGICCGTCTGCAGAGTGTGAACATITG 813  DA 1 AIGCGAGCTGGAAAGTGICAACATTTG 813	Qy	1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
814 CGGATCCGGGAGTGCACCCCCCGAGAATGGGGGCAATTCTGTGAAGTTTA 87 817 CGGATCCGGAGTGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 87	\$ g	1894 GGGACCTATGCGCTCACTGGACAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953 
874 AGCCAGGATCTGAAAACTGCACACACACTTTTGCATCATAAAAAAAA	oy O	1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTG 2013
934 GARATARARACCCCAAAGCATTGAGAAGGCCAGCCAGCCTTGTACTCGGGCTTGGGT	oy da	2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGCACGG 2073 
224GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 994 GCTGCGTCGTGGCGTTGCAGTCCTTGGTGTCACCCTTTACAGAGCAG	λ O	2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
DD 2.68 GCTGCCGTCGTGGGCCGTTGCAGTCCTGGTCATCGCCCTTTACAGACGGAGCCAG 3.27  Qy 1054 AGTGACTATGGCGTGGACGTCATTGACTTCTGCATTGACGGGCTGGCT	S G	2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGC
1114 AACTTCAAACCGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCAAGAAAAAAAA	Qy	2194 CCGTTCTCCCGCGTGTGGTGCTAACCGGCGCCCTGCACTGTGCCTTCTCCCTGGGG 2253
1174 THIGGIAACTCCCTGCTCCTGAATTCTGCCAGCCAGATCTGACAGTGACCGGACAAAAAAAA	Qy	2254 CGTTATACGCCCACTACCACCTGCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313 
1234 TACAGCGAACCCATCTGTCTGCAGAACCTCTTGGACAAGGAGGTCATGACAGAGTCCTCA 508 TACAGCGAACCCATCTGTCTGCAGAACCAACAACAACAACAACAACAACAACAACAACAA	ςς Dp	2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373 
1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGGTCGGTC	S ea	TICTICGCACAAGGACAGCACTITICCCIGCACAGACTGGCCCCAAAGCCTICAAAATI 
Oy         1354 GGAGTGTCTGAGAGAGCTGAGGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413           Db         628 GGAGTGTCTGAGAGACTCACGCCAAGAATCATTCCAGGACTTTTCCCCATGGA 687	oy da	249
1414 AACAACCACAGCTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCAAAATCTG	S q	2494 GACTGGCAGNIGITAGCACAGAAAAAGCATGACAGAATTTATCTTATTTGGCTACA 2553 

421 AACTTCAAAACAGTCCGTCAA	1714   ACTCCCTTTGCATTGACCATCGCGCACTGGCGGTGTCAGTCTCAGCATTGGAATATC   1773
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Qy   2554   CAMAGTAGCCCATCTGCTGTCATTTCAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613	Query Match         71.2%; Score 1949; DB 4; Length 2001;           Best Local Similarity         97.3%; Pred. No. 0;           Matches 2001; Conservative         0; Mismatches         0; Indels         42; Gaps         1;           Qy         694 ATGGCAGCAACATCGTGGCTAAGAGGAAGAGCTGTGGCCACTGTTGTGGTCTACGTG         53           Db         1 ATGGCAGCCAACATCGTGGCTAAGAGGAGGAGGCTGTGGCCACTGTTGTGGTCTACGTG         53           Db         754 GATGGGAGCTGACACTGGGCTGAACACTGTGGGCCACTGTTGGTGTGAACATTG         813           Call

121 CGGATCCGGGAGTGCACCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180 874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933 181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG	934 GAAATAAAACCCCAAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993 224	994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATCGCCCTTTACAGACGGAGCCAG 1053 268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATCGTGTCACCCTTTACAGACGGAGCCAG 327			TITGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCGGACA-GGTAACTCCTGCTCTGAATTCTGCCATGCAGCCAGATCTGACCGGACA			1354   GGAGTGTCTGAGAGAGCTGAGTACCAGGGAAGAATCATTCCAGGACTTTTCCCCATGGA   1413	1414 AACAACCACAGGTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCG 1473 	1474 TCATCACTCCCCACAAGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533 	1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACACGTGCCATCCCAGAG 1593 	1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653 	1654 GGCTCTGAGGTGCTCCTGAGTCCTGAGGTCCTCCAGACATGATCGTCGCC 1713	1714 ACTCCTTTGCATTGACCACCGGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773	183	112	1894 GGGACCTATGCGCTCACTGGAGGCCAATCACAGACTGTGCCGTGAAGGAACTGAAGGTG 1953 
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CGTTATACGCCCACTACCACCTGCTGCTGCAAATCTGCATTCGGCAGCTCAAAGGC 2	CATGAACAGATCCTCCAAGTGCAGACATCCTAGAGAAGTGAACAGAGAAACCATCATCATCTCCAAGAGCAACCGAAGAGCAACCATCAATCCTAGAGAGAACGAAGCCATCAATCCTAGAGAGAACGAAGAGAACCATCAATCCTAGAGAGAACGAAGAGAAACCATCAATCCTAGAGAGAACGAAGAAACCATCAATCA	2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2 1639 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTCGCCCCAAAGCCTTCAAAATT 1	2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2	2494 GACTGGCAGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTGGCTACA 2 	2554 CAAAGTAGCCCATCTGCTGTTTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2	2614 GAICTIGACTCCCTGGCCTTTGAAGAGAITGGGGAGGACACACACGAAACTCTCA 2	2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2	2734 TAG 2736         1999 TAG 2001	RESULT 9 US-09-969-532-31 ; Sequence 31, Application US/0969532		Human Membrane Proteins and Polynucl '969,532	PRIOR APPLICATION NUMBER: US 60/237,280 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 33 SOFTWARE: PastSEQ for Windows Version 4.0	SEQ ID NO 31 LENGTH: 1968 TYPE: DNA ORGANISM: homo sapiens	5%; Score 1873; DB 4; Length 1968; 3%; Pred. No. 0;	vative         0; Mismatches         0; Indels         75; Gaps           AACATCGTGGCTAAGAGAGAAAGCCTGTGGGCACTGTTGTGGTCTACGTG         0; Indels         0; Indels	TTTG 	CGGATCCGGGAGTGCACCACCCCGGGGAAATGGGGGCAAATTCTGTGAAGGTTA

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                                                             59.9%; bccc. No. c, 100.0%; Pred. No. c, 0; Mismatches
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                     TYPE: DNA
CRGANISM: homo sapiens
US-09-969-532-1
                                                                                Similarity
SEQ ID NO 1
LENGTH: 1734
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Matches 1640;
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APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
TITLE OF INVENTION: No. 677232el Human Membrane Proteins and Polymucleotides Encodin
FILE REPERENCE: LEX-024-40.02
CURRENT APPLICATION NUMBER: US/09/969,532
CURRENT PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 60/237,280
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 1, Application US/09969532
Patent No. 6777232
GENERAL INFORMATION:
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Matches 1607;         Conservative         0;         Mismatches         0;         Indels 33;         Gaps 1;           Qy         1         ATGGGGAGAGCGGCGCGCGGGGGGGGGGGCGCGCGCGCGC	181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGGGGAGGCCAGCC 241 ATGCAGATATTCTTCAAATGCAACGGGAGTGGGTCCATCAGAACGACACGTCTTGAA 241 ATGCAGATATTCTTCAAATGCAACGGGAGTGGGTCCATCAGAACGACACGTCTCTGAA 301 GAGACTCTGGAGCAGAGGTCCAGGATGGGTCCATCACAAAGTTCATAGAGTCCAGGAAGAGTTCATCATAGAGTTCAAGGTCCGGGAAGTTTCATCAATGTTACTAGG	361 361 421 481	541 541 601 601 601 601	721 A 721 A 721 A 781 I 781 I 841 C 901 G 901 G 928 C
Qy         961         GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGTGCGTTGCAGTCCTG         1020           Db         961         GCCAGCGACATTGCTTTGTACTCGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	OY 1141 AATATCATGGAACTAATGATACAAGAAAATCCTTTGGTAACTCCCTGCTCCTGGAATTCT 1200	Oy 1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTTCAGAGAGCTGAGTACCAC 1380  Db 1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGGAGCTGAGTACCAC 1380  Qy 1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACAGCTTTAGTACAATGCAT 1440  Db 1381 GGCAAGAATTCATCCAGGACTTTTCCCATGGAAACAACACACAC	QY         1501 AGGACAACTGGTGTTTTGGCCATTTAGGGGGGGCCTTAGTAATGCCAATACAGGGTG 1560           Db         1501 AGGACAACTGGTGTTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560           QY         1561 AGCTTACTCATACCACAGGTGCCATCCCAGAGGAATTCTTGGGAGATTTATATGTCC 1620           Db         1561 AGCTTACTCATACCACAGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620           QY         1621 ATCAACCAAGGTGAACCCAG 1640           Db         1621 ATCAACCAAGGTGAACCCAG 1640           Db         1621 ATCAACCAAGGTGAACCCAG 1640	RESULT 11 US-09-96-512-3 US-09-969-512-3 Sequence 3, Application US/09969532 Fatent No. 6777232 FAPLICANT: Walke, D. Wade FILIS REPERENCE: LEX-0244-USA FILIS REPERENCE: LEX-0244-USA CURRENT APPLICATION NUMBER: US/09/969,532 CURRENT FILING DATE: 2000-10-02 FRIOR APPLICATION NUMBER: US 60/237,280 FRIOR APPLICATION NUMBER: US 60/237,280 FRIOR PILING DATE: 2000-10-02 FRIOR PILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR PILING DATE: 2000-10-02 FRIOR PILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR PILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR FILING DATE: 2000-10-02 FRIOR PILING DATE: 2000-10-03 FRIOR FILING DATE: 2000-10-0-03 FRIOR FILING DATE: 2000-10-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-

CTGGGGCTGTGCTTCTGGGCGGCGGGGGCTGCCCGAGGAACTGACAATGCGGAA GCCTTCCCGAATCCATCCATCAGCTCCTGGGACCTGCCTG	721 AGAAGCCTGTCGGCCATGTTGTGGTCTACGTGGATGGGAAGTGTGGAAGCGAA 780 781 TGGTCCGTCTGCAGGTCTGAACATTTGCGGATCCGGGAGTGCACACCACCCC 840 781 TGGTCCGTCTGCAGGTCTGAACATTTGCGGATCCGGGAGTGCACACACCACCCC 840 781 TGGTCCGTCTGCAGATTCTGTGAACATTTGCGGATCCGGGAGTGCACACACCCCC 840 841 CCGAGAAATGGGGGCAAATTCTGTGAAGTCTAAGCCGGAATCTGAAAACTGCACACAC 841 CCGAGAAATGGGGGCAAATTCTGTGAAGTCTTAAGCCGGAATCTGAAAACTGCACACAC 841 CCGAGAAATGGGGGCAAATTCTGTGAAGTCTTAAGCCAGGAATCTGAAAACACCCCAAAGCATTGAGAAT 900 901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAAACCCCAAAGCATTGAGAAT 960 901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAAACCCCAAAGCATTGAGAAT 960 901 GGTCTTTGCATCTTGTACTCGGGCTTGGGTGCTGCCGTGGCTTGCAGTTCTTG 1020 1021 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTTGCAGTCTTG 1020 1021 GTCATTGGTGCTTTGTACTCGGGCTTGGGTGCTGCTGGCCGTTGCAGTCCTTG 1020 1021 GTCATTGGTGCTCACCTTTACAGACGAGGCTTGCAGTGCTTGCAGTCCTTGAGTTGACTTGAGTGCTTTGGTGCTTTGGTGCTTTGGTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTGACTTTGATTGA
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1081 TCTTCTGCATTGACAGGTGCCTTCCAACCTTCAACTTCAAACAGTCCGTCAAGCCAAG 1140	Parent No. 6777232  GENERAL INFORMATION: APPLICANT: Walke, D. Wade APPLICANT: Scoville, John TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polymucleotides Encodin FILE REPRENSE: EEX-0244-012A CURRENT APPLICATION NUMBER: US 60/237,280 PRIOR APPLICATION NUMBER: US 60/237,280 PRIOR PILING DATE: 2000-10-02 PRIOR PILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 33 SEQ ID NOS: 33 SEQ ID NO 5 LENGTH: 1692 TYPE: DNA ORGANISM: homo sapiens US-09-969-532-5  QUETY MATCH Best Local Similarity 97.4%; Pred: No. 0; Matches 1598; Conservative 0; Mismatches 0; Indels 42; Gaps 1; MATGGGGAGAGCGGCGCCACCGCAGGGGGGGGGGGGGGGG

181 GATGATGCTTATATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240 241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300	STTACTAGG 3				541 CGCCCACCAGAGGGGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600 	601 GACTCTGAACGAGGAGGACATTGACACCAGGGCTGACCATAACCTGATCATCAGGGAG 660 	661 GCACGGCTCTCGGACTCCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720 	721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGAGGGGGGAGCTGGGGAAGTGTGGAGCGAA 780 721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780	781 TGGTCCGTCTGCAGACAGAGAGATTGCGGATCCGGAGTGCACACACCCC 840 	841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900 	901 GGTCTTTGCATCCTAGATAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960 	961 GCCAGCGACATTGTACTCGGGCTTGGGTGCTGCCGTCGTGCGTTGCAGTCCTG 1020 928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTTGCAGTCCTG 987		1 TCTTCGCATGCATGCGCAAGGGCCAAGGGCAAGGTCCAAAACAGTCCGTCAAGCCAAG 11	1048 TCTTCTGCATTGACAGGTGCCTTCCAACTTCAAAAAAAACGTCCGTC		1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTTGCAGGAC 1260 	- w
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OY 1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTG	Oy 1261 CCTCTGGACAAGAGCTCATGACAGAGTCCTCACTTTAACCCTTTGTGGACATCAAA 1320 	Qy 1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380	OY 1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTAGTACAATGCAT 1440	Qy 1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500	OY 1501 AGGACAACTGGTGTTTTGGCCATTTAGGGGGGCGCTTAGTAGTAATGCCAAATACAGGGGTG 1560	QY 1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGAGAATTCTTGGGAGATTTATATGTCC 1620	OY 1621 ATCAACCAAGGTGAACCCAG 1640  Db 1579 ATCAACCAAGGTGAACCCAG 1598	RESULT 13 US-09-969-532-7 Seminance 7. Application US/09969532		5663	PRIOR FILING DATE: 2000-10-02  NUMBER OF SEQ ID NOS: 33  NUMBER OF SEQ ID NOS: 33  NUMBER OF SEQ ID NOS: 33	בוומסמים מבוים בי	<pre> ; ORCANISM: homo sapiens US-09-969-532-7 Query Match 53.7%; Score 1470; DB 4; Length 1659;</pre>		Oy 1 ATGGGGAGGGGGCCACCGCAGGGGGGGGGGGGGGGGGGG	61 CTGGGGCTGTGCTTCTGGGCGGCGGGGGCTGCCCGAGGAACTGACAATGGCGAA 12	Db 61 CTGGGGCTGTGCTTCTGGGCGGCACCGCGCCTGCCCGAGGAACTGACAATGGCAAA 120 Oy 121 GCCCTTCCCGAATCCATCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGACCA 180	Db 121 GCCTTCCCGAATCCATCCATCAGCTCCTGGGACACTGCCTATTCATAGAGGAGCCA 180  Qy 181 GATGATGCTTATATATCAAGAGCAACACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Db 301 GCTGCCGTCGTCGCCGTTGCAGTCCTTGGTGTCACCCTTTACAGACGAGCCAG 360  Oy 1054 AGTGACTATGGCGTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113  Db 361 AGTGACTATGGCGTGGACGTCATTGACTTCACAGATGGCTTCCAGACCTTC 420  Oy 1114 AACTTCAAAAAAGTCCGTCAGACCAGAATTATAGAAAAAAACC 1173  Db 421 AACTTCAAAAACAGTCCGTCAGACCAGAATATCATGGAACTTACAAGAAAAAACC 1173		FARENAL INFORMATION:   APPLICANT: Walke, D. Wade
0y         1321         GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGCTGACTACCAC         1380           1246         GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGACTCACCAC         1305           0y         1381         GGCAAGAATCATCCAGGACTTTTCCCCTGGGAACAGCTTTAGTACAATGCAT         140           1306         GGCAAGAATCATTCCAGAGCTTTTCCCCATGGAACACCACAGCTTTAGTACAATGCAT         136           0y         141         CCCAGAAATAAAATGCCCTACATCCATGGAACAACACACAC	RESULT 14 US-09-969-532-17 is Sequence 17, Application US/09969532 is Batent No. 6777232 is Cantened No. 6777232 is Cantened No. 6777232 is Cantened No. 6777232 is Cantened No. 6777232 is APPLICANT: Walke, D. Wade is APPLICANT: Walke, D. Wade is APPLICANT: Walke, D. Wade is TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polymucleotides Encoding TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polymucleotides Encoding TITLE OF INVENTION: No. 6777232e1 is RILE REFERENCE: LEX-0244-USA is CURRENT FILING DATE: 2001-10-02 is PRIOR PILING DATE: 2001-10-02 is PRIOR PILING DATE: 2000-10-02 is NUMBER OF SEQ ID NOS: 33 is SOFTWARE: PastSEQ for Windows Version 4.0 is SEQ ID NO 17 is LENGTH: 1041 is TYPE: DNA is ORGANISM: homo sapiens US-09-969-532-17	Query Match         34.6%; Score 947; DB 4; Length 1041;           Best Local Similarity 100.0%; Pred. No. 1.36-289;         Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;           Qy         694 ATGGCAGCCAACATCGTGGCTAAGAGGAAAGCCTGTGGGCCATGTTGGGTCTACGTG 53           Db         1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCTGTGGGCCATGTGGGTCTACGTG 60           Qy         754 GATGGGAGCTGAACATCGTGGAGCATGCTGCAGTCTGTGGTGTATTG 813           Db         61 GATGGGAGCTGGAGAGTGGAGCGAATGGTCGAGTCTGCAGTCTGTGGTGTATTG 120           Qy         754 GATGGGAGTGGAGCAATGGTCCGTCTGCAGTCTGAAGTTTG 813           Db         61 GATGGGAGTGCAGAGCACCCCCCCGAGAATGGGGGCAAATTCTGTGAAGGTCTA 873           Db         121 CGGATCCGGGAGTGCACACCCCCCCGGGAAATGGGGGCAAATTCTGTGAAGGTCTA 180           Qy         874 AGCCAGGAATGGACCACACCCCCCCGAGAAATGGGGGCAAATTCTGTAGAAGTCTA 180           Db         121 CGGATCCGGGAGTGCACACACACACACACACACACACACA

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Search completed: April 1, 2005, 05:46:11 Job time : 467 secs

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    10937.661 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 9, Appli	Sequence 33, Appl	Sequence 11, Appl		15,		Sequence 136, App	Sequence 55, Appl			Sequence 25, Appl
ΩΙ	US-10-798-721-9	US-10-798-721-33	US-10-798-721-11	US-10-798-721-13	US-10-798-721-15	US-10-723-860-7444	US-10-473-518-136	US-10-872-681-55	US-10-094-886-115	US-10-872-681-53	US-10-798-721-25
DB	18	18	18	18	18	18	18	19	17	19	18
* Query Match Length DB	2736	3411	2703	2694	2661	8899	2979	2868	2898	2661	2043
* Query Match	100.0	100.0	97.2	96.6	93.8	84.8	83.6	83.5	82.6	81.1	74.7
Score	2736	2736	2660	2642	2566	2320.8	2287	2284	2260	2220	2043
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## ALIGNMENTS

US-10-798-721-9

US-10-798-721-9	6.1
; Sequence 9,	Sequence 9, Application US/10798721
, Publication	Publication No. US20040248166A1
; GENERAL INFORMATION:	ORMATION:
; APPLICANT:	APPLICANT: Walke, D. Wade
; APPLICANT:	APPLICANT: Scoville, John
, TITLE OF I	TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFER	FILE REFERENCE: LEX-0244-USA
; CURRENT AP	CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FI	CURRENT FILING DATE: 2004-03-11
; PRIOR APPL	PRIOR APPLICATION NUMBER: US/09/969,532
, PRIOR FILI	PRIOR FILING DATE: 2001-10-02
; PRIOR APPL	PRIOR APPLICATION NUMBER: US 60/237, 280
; PRIOR FILL	PRIOR FILING DATE: 2000-10-02
, NUMBER OF	NUMBER OF SEQ ID NOS: 33
; SOFTWARE:	SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9	
; LENGTH: 2736	736
; TYPE: DNA	
, ORGANISM:	ORGANISM: homo sapiens
US-10-798-721-9	6-
Query Match	100.08;
Best Local Similarity Matches 2736: Conserv	Best Local Similarity 100.0%; Pred. No. 0; Matches 2736: Conservative 0: Mismatches 0: Indels 0: Gaos 0:
0y 1	1 ATGGGGAGAGCGGCGCACCGCAGGCGGCGGCGGGGCGCGCGCGCTGGCTCCCGTGG 60
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; Publication No. US20040248166A1
; GENERAL INFORMATION:
    APPLICANT: Walke, D. Wade
; APPLICANT: Walke, D. Wade
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the $
; FILE REFERENCE: LEX. 0244-03-11
; PRIOR PELLING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FRSESEQ for Windows Version 4.0
; SEQ ID NO 33
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100.0%; Score 2736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches
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CORGANISM: homo sapiens
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Oy 2401 CCTGCACAGACTGGCCCCAAAGCTTCAAAATT  Db 2515 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATT  Oy 2461 GCTACATTTGATACCCCCAAAGCCAC  Oy 2521 AGCATCAATTGATACCCCCAAAGCCAAC  Oy 2521 AGCATCAACAGGAATTTATCTTATTTCGCTACA  Oy 2581 AACCTGTGGGAAGTTTATCTTATTTCGCTACA  Oy 2581 AACCTGTGGGAAGCTCGTCATCACAGCATGATGGT  Oy 2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 AACCTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 CAACTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 CAACTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 CAACTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 CAACTTGTGGGAAGCTCGTCATCAGCATGATGGT  Oy 2695 CAACTTGTGGGAAGCTCGTCATCAGCATGATGGTTCTCTCTC		Db 61 CTGGGGTTTTTTGGGGGGGGGGGGCGGGGCGGGGCGGG
1321   GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGCTGACTACCAC   1380   1435   GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTTGAGAGCTGACTACCAC   1494   1435   GTGAAAGTCCAGAGCTTCTCCAGGAGTGTCTTGGGAACATACCAC   1494   1495   GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACACACAC	1681 GTCACCTGTGGTCCTCCAGACATGATCCACCACCCCTTTGCATTGACCATCCCGCAC	
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roteins and Polynucleotides Encoding the S CACAAAGTAGCCCATCTGCTGTCATTTTG 2580 HORATCTTGACTCCCTGGCCTGTGCCCTT 2640 CAAACATTTCAGAATCCCAGCTTGATGAA 2700 TICCCTACTCCATCAGACAGCGGATITGT 2460 AGGACTGGCAGATGTTAGCACAGAAAAAC 2520 GGACACTGCTTTCATAGAGGAGCA 180 ATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240 STCCGCGAAGTGTTCATCAATGTTACTAGG 360 ); nes 0; Indels 33; Gaps DB 18; Length 2703; CTCTAG 2736 |||||| CTCTAG 2850

421 421 481 541 541		Db 721 AGAAGCCTGTGGGCTGTTGTTGTTGTTTTTGTGGATGGGAGTGTGGGAGTGGGAGCGGAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGAGTGGAGTGCAGAGTGCAGAGTGTGAAACTTTGCGGATCCGGGAGTGCACACCACCCCCCCC	901	1021 1021 1081	1001 1141 1135 1201	1159 1261 1219	1321 GTGAAGTCCAGAGCTTGTTTTCCTGGGAGTGTCTGAGAGAGTGAGT	Qy 1441 CCCAGAAATAAAATGCCTACATCCAAAATCTGTCATCACTCCCCCACAAGGACAGAACTC
2521 AGCATCAACAGGAATTTATCTTATTTCGCTACAAAGTAGCCCATCTGCTGTCATTTTG 2580 2488 AGCATCAACAGGAATTTATCTTATTTCGCTACAAAGTAGCCCATCTGCTGTCATTTTG 2547 2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGATCTTGACCCCTTGCTGCTGTTTTTG 2547 2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640 2548 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCTGGCCTGTGCCCTT 2607 2641 GAAGAGATTGGGAAGCACACACGAAACTCTCAAACATTCAGAATCCCAGCTTGATGAA 2700 2668 GAAGAGATTGGGAAGGACACACGAAACTCTCAAACATTTCAGAAATCCCAGCTTGATGAA 2667	2701 GCCGACTTCAACTACAGCAAAATGGACTCTAG 2736 2668 GCCGACTTCAACTACAGCAAAATGGACTCTAG 2703 -721-13 -721-13 -721-13	ne Proteins and Polynucleotides Encoding th 721 2	PRIOR APPLICATION NUMBER: US 60/237,280 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 13 LENGTH: 2694 TYPE: DNA ORGANISM: homo sapiens	US-10-798-721-13  Query Match 96.6%; Score 2642; DB 18; Length 2694;  Best Local Similarity 98.5%; Pred. No. 0;  Matches 2694; Conservative 0; Mismatches 0; Indels 42; Gaps 1;  Qy 1 ATGGGGAGGCGGCGCGCGCGCGGGGGGGGGGGGGGGGGG	SCGCCACCGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	121 GCCCTTCCCGAATCCATCCATCAGCTCCTGGGACACTGCCTTTCATAGAGGAGCCA 180 181 GATGATCTTATTAAGAGCAACCCTATTGCACTCAGTGCAAACGAGGCCAGCC 240 181 GATGATTATTATTAAGACAACCCTATTGCACTCAGTTGCAAAGCGAGGCCAGCC 240 181 GATGATGTTATTATAAGAGAACCCTATTGCACTAGTTGCAAAGCGAGGCCAGCC 240	ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA	301 GAGACTCTGGACGAGAGCTCTGAGGTTTGAAGGTCCCGCGAAGTGTTCATCAATGTTACTAGG 360 361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATGGTGCCGGTGTGTGCGTGGAGGC 420 111111111111111111111111111111111111

qq		2539 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCTT 259
<u>ራ</u> 8	1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGAGAATTCTTGGGAGATTTATATGTCC 1620	
& B	1621 ATCAACCAAGGTGAACCCGGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680	Db 2659 GCCACTTCAACTACAGCAAAATGGACTCTAG 2736  Db 2659 GCCACTTCAACTACAGCAGCAAAATGGACTCTAG 2694
& a	1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740	RESULT 5 US-10-798-721-15 ; Sequence 15, Application US/10798721
දු පු	1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800 	PUDIICATION NO. USZU040248166A1 GENERAL INFORMATION. APPLICANT: Walke, D. Wade APPLICANT: Scoville, John
& a	1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860 	; TILLE OF INVENTION: NOVEL HUMAN MEMOFANE FIOCEINS AND FOLYNUCLEOLIDES ENCOQUING THE S.; CURRENT APPLICATION NUMBER: US/10/798,721 ; CURRENT FILING DATE: 2004-03-11
දු පු	1861   CCCTTTGCGTGTCATGTGCTCCTGGACCCTTTGGGACCCTATGCGCTCACTGGAGAGCCA	; PRIOR APPLICATION NUMBER: US/09/969,532 ; PRIOR PLING DATE: 2001-10-02 ; PRIOR FILING DATE: 2000-10-02 ; PRIOR FILING DATE: 2000-10-02
SP GS	1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980	; NOWMER OF SEQ 1D NOS: 33 ; SOFTWARE FastSEQ for Windows Version 4.0 ; SEQ 1D NO 15 ; LENGTH: 2661
දු පු	1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040 	
<u>ئ</u> ۾	2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCTT 2100 	Query Match 93.8%; Score 2566; DB 18; Length 2661; Best Local Similarity 97.3%; Pred. No. 0; Matches 2661; Conservative 0; Mismatches 0; Indels 75; Gaps 2;
<i>à</i> 8	2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160	QY         1 ATGGGGAGAGGGGCGCCACCGCAGGGGGGGGGGGGGCGCCGC
3 8 8	AGAITHANACCATTCACTGCTGCAGAGATTCTGCCTGTGTGCCCCGTTCTGCCCTTTGCCTGTGCCCTTTTGCCTGTGCTGTGTGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGT	OY 61 CTGGGGCTGTGCTTCTGGGCGGGAGGGCCGCGGGGGGAGCTGACAATGGCGAA 120
3 8 8	AGAGAGCCCTGCATTCACTGCCTGCCAGGAAGTCCCCGTTATTACGCCCGGGGGGGG	Oy 121 GCCTTCCCGAATCCATCACCTCGGGACACTGCCTCATTCAT
8 8 8	TCTGGAAAATCTGGATTGGGGAGCTGAAGGGCATGAAGGGCATGAGGGGAAGAGGGGAAAATCTGGATTGGGAGGCTAAAGGGCGATGAAAAAGATCCTCCAAGTGGAGAGAAAATGAAAGAAA	OY 181 GATGATGCTTATATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
8 8 8	TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAGAGGACAGCACTTTC 24	OY 241 ATGCAGATATTCTTCAAATGCAACGGGGGTCCATCAGAACGAGCACGTCTCTGAA 300
8 8 8	CCTGCACACACCCCCAAAGCCTTCAAATTCCCTACTCCATCAGACAGA	OY 301 GAGACTCTGGAGGGTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
8 & 8	CCTACATTGATACCCCCAATGCCAAGGCAAGGACTGGCAGAGTGTTAGCACAGAAAAC 25	Oy 361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGGCGTGGAG 420
8 8	AGCATCAACAGGAATTTATCTTATTTCGCTACAAAGTAGCCCATCTGCTGTCATTTTG 25	OY 421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
8 &	ACCTGTGGGAACTCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	Qy 481 TTTGAACAAGAAGGAAGGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

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1149 AACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCG 1208
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       AGGACTATTGGTGCCAGTGTGTGTGGCGTGGAGCCACTGGGTACCTCCAAGAGCAGGAAGG 488
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                                                       TTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCG
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                                                                                                                                Sequence 7444, Application US/10723860

Publication No. US20040255606A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alatsaha
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: 108/10/723,860
CURRENT PILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 7444

LENGTH: 8899
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OTHER INFORMATION: n is a, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (2173)..(2189)
OTHER INFORMATION: n is a, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (2947)..(2972)
OTHER INFORMATION: n is a, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (5055)..(5069)
OTHER INFORMATION: n is a, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (5055)..(5069)
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LOCATION: (7333)..(7336)
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Matches 2552; Conservative
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Oy 2441 CCATCAGACAC Db 2607 CCATCAGACAC Oy 2501 AGATGTTAGG Db 2667 AGATGTTAGG Oy 2561 GCCCATCTGG	2621 2621 2787 2681 2847	RESULT 7 US-10-473-518-136 US-10-473-518-136 Sequence 136, Applicat. Publication No. US2004 GENERAL INFORMATION: APPLICANT: THORNTON, APPLICANT: THORNTON, APPLICANT: RICHARDSO APPLICANT: RICHARDSO APPLICANT: RICHARDSO APPLICANT: RAILICK. APPLICANT: RAILICK.			SE S
1361 CTGAGAGACTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAAC 1420 1527 CTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAAC 1586 1421 ACAGCTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1480 1587 ACAGCTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1480 1587 ACAGCTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCCAAAATCTGTCATCAC 1646 1587 ACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATTAGGGGGGGG				1961 TTGGCTGCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGACAATA 2020 2127 TTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGACAATA 2020 2127 TTGGCTGCATTTCAGAAGTTTCAGATTACAAGTGAAGGCATTAANNNNNNNNNN	
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	ò	2034 TCAGGAAGIGGTTTCAGAIGAAAGGCAICAAGGIGGACAGCTCCTGGAAGAACAACCAAAIT 2093		Matche	8 2557;	CO
	qq	2238 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2297		ò	102 A	AGGAAC
	'n	2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2153		qq	144 AGGAAC	3GAAC
	DP	2298 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2357	•	λ̈́o	162 T	TCATT
	ò	2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213		đ	204 T	TCATT
	q	2358 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCCGTTCTCCCGGGTGGTG 2417		Š	222 G	GTGCA
	ò	2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273		qq	264 G	GTGCA
	qq	2418 CAGTAACCGGCAGCCCCTGCACTGCCTTCTCCCCTGGAGCGTTATACGCCCCACTACCAC 2477		λō	282 _	GAACG
	δý	2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333		qq	324 G	GAACG
	Ор	2478 CCAGCTGCCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2537	· ·	δλ	342 G	GTTCA
	ò	2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393		qq	384 G	GTTCA
	qq	2538 GCAGACATCCATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2597		ολ	402 C	CCAGT
	ò	2394 CACTTTCCTGCACAGACTGGCCCCAAAGCTTCAAAATTCCCTACTCCATCAGACAGCG 2453	· <u>-</u>	qa	444 C	CCAGT
	qa	2598 CACTTICCCTGCACAGACTGGCCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2657	-	ò	462 A	AGCCT
	ζŏ	2454 GATTTGTGCTACATTTGATACCCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2513	_	qq	504 A	AGCCT
	qq	2658 GATTTGTGCTACATTTGATACCCCCAATGCCAAGGCAAGGAAGG		δλ	522 C	CATGA
	λ̈́o	2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2573		qq	564 C	CATGA
	QQ	2718 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACAAAGTAGCCCATCTGCTGT 2777		ò	582 G	GAAAA
	ò	2574 CATTITGAACCIGIGGGAAGCICGICAICAGCAIGAIGGIGAICCIIGACICCCIGGCCIG 2633		Ωp	624 G	GANAA
	qq	2778 CATITICAACCTGTGGGAAGCTCGTCATCAGCATGATGTGATCTTGACTCCCTGGCCTG 2837		ò	642 T	TAACC
	ò	2634 IGCCCTTGAAGAGATTGGGAGGACACACACAAAACTCTCAAACATTTCAGAATCCCAGGT 2693		ΩÞ	684 T	TAACC
	qq	2838 TGCCCTTGAAGAGATTGGGAGGACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2897		οy	702 C	CAACA
	λō	2694 TGATGAAGCCGACTTCAACTACAGCAAGCCAAAATGGACTCTAG 2736		ΟP	744 C	CAACA
	ΩÞ	2898 TGATGAAGCCGACTTCAACTACAGGAAAATGGACTCTAG 2940		ò	751 -	1
				ΩĐ	804 C	CTGGT
		872-681-55		ò	751 -	;
	; Sequen ; Public	Sequence 55, Application US/108/2681 Publication No. US20050026251A1	_	QQ	864 A	ACGTT
	GENER?	RAL INFORMATION: LICANT: ARES TRADING LIMITED		ò	751 -	
	, TITLE ; FILE	TE OF INVENTION: TRANSMEMBRANG PROJEIN E REFERENCE: P029209WO		đ	924 G	GTCAG
	; CURRE	CURRENT APPLICATION NUMBER: US/10/872,681 CURRENT FILING DATE: 2004-06-21		ò	774 G	GAGCG
	, PRIOR , PRIOR	OR APPLICATION NUMBER: GB0130721.4 OR FILING DATE: 2001-12-21		<del>Q</del>	984 G	GAGCG
	SOFT'S	NUMBER OF SEQ ID NOS: 56 SOFTWARE: SegMin99, vergion 1.02		ò	834 A	ACCAC
	SEC II	Q ID NO 55 LIENCHH: 2868		Ор	1044 2	ACCAC
	ORG	11FE: DNA ORGANISM: Homo sapiens		ζ,	894	CACAG
•	; NAME ; NAME US-10-87	, FEATURE: ; NAME/CKE: SEQ ID NO:33 US-10-872-681-55		qq	1104	CACAG
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|GATGGTCTTTGCATCCTAG-----GCAT
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                                                                       ACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCTCCACGGCTCCTGGGACACTGCC
                            Gaps
                         0; Indels 243;
Length 2868;
   DB 19;
 83.5%; Score 2284; Dirity 91.3%; Pred. No. 0; onservative 0; Mismatches
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462   MCCCINTTACCGANALACTICANCAGACCCACAGGAAGGCAACTICCCATTCANGG 511   458   MCCCINTTACCGANALACTICACCCACAGGAGGAACTICCCATTCANGG 512   458   MCCCINTTACCGANALACTICACCCCACAGGAGGAACTICCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCCAGGAGGAACTICCCTCCAGGAACTICCCTCCCAGGAGGAACTICCCAGGAGGAACTICCCTCCAGGAACTICCCTCCAGGAACTICCCTCCAGGAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCCAGGAACTICCAGGAACTICCCAGGAACTICCAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGGAACTACAGAACTACAGAACTACAGAACTACAGAACTACACAGGAACTACACAGAACTACACAGAACTACACAGAACTACACACAC	Db 1436 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1495
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APPLICANT: Seathmen, Glemada APPLICANT: Gerhuen, Valoria A	Db 398 CCAGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAAGGCCTCTGTGCGCAT 457

255 CONTRICTABLE C
246 CCCAMTCCAMAGCAMGATTGCAMATTGCAMACTAGCAMACAGATTGCAMAGCAMA
2355 [TANTITION CONTRACTORAGE CONTRACTORAGE AND MAINTENED CONTRACTORAGE

814 CGGATCCGGGAGTGCACCACCCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873 	874 AGCCAGGAAICTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933	934 GABATABARCCCCAAAGCATTGAGAATGCCAGGGACATTGCTTTGTACTCGGGCTTGGGT 993	994 GCTGCCGTCGTGGCCGTTGCAGTCCTTGGTGATCACCCTTTACAGACGGAGCCAG 105:	1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 111:	1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1177 		1234 TACAGCGGACCCATCTGTCTGCAGGACCTCTGGACGAGGAGCTCATGACAGAGTCCTCA 129:	1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 135:	1354 GGAGTGTCTGAGAGGGGAGTACCAGGGAAGATCATTCCAGGACTTTTCCCCATGGA 1413	1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473	1474 TCATCACTCCCCACAAGAACAGAACTGAGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533	1534 CGCTTAGTAATGCCAAATACAGGGTGAGCTTACTCATACCACGGTGCCATCCCAGAG 159:	1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACGAGGTGAACCCAGCCTCCAGTCAGAT 165:	1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713	1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1777	1774 CATTTAAAGAAGAGACACAGCAGGGCAAATGGGGAAGGAA	1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 189:	1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCCGTGAAGCAACTGAAGGTG 195
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 2001
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Best Local Similarity 97.9%;
Matches 2001; Conservative
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1 Sequence 29, Application US/10798721

2 Sequence 29, Application US/10798721

3 Sequence 29, Application US/10798721

3 EDBEAL INFORMATION:

4 APPLICANT: Walke, D. Wade

7 TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the CURRENT APPLICANTION NUMBER: US/10/798,721

5 CURRENT APPLICATION NUMBER: US/09/969,532

7 TITLE OF INVENTION NUMBER: US/09/969,532

7 PRIOR APPLICATION NUMBER: US/09/969,532

7 PRIOR FILING DATE: 2001-10-02
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<u>ځ</u> ځ	1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653	OY 2674 AACAITICAGAAICCCAGCTIGAIGAAGCCGACTICAACIACAGCAAAAIGGACTC 2733
3 & a	4 GGCTCTGAGGTGCTCCTGAGTCCTGTGCTGCTCCTCCAGCCTCCAGCTCAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	Qy 2734 TAG 2736 Db 1999 TAG 2001
දු පු	1714 ACTCCCTTTGCATTGACCATCCGCACTGTGCAGATGTCTGAGGATTGGAGATATC 1773	യഗ
& 8	1774 CATTTAAAGAAGACACAGGCAGAGGGCAAATGGGAGGAAGTGATGTCACTGGAAGATGAA 1833 	PUDIICATION NO. USZU040248166A1 GENERAL INFORMATION APPLICANT: Walke, D. Wade APPLICANT: Scoville, John
දු පු	1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893	
රු සි	1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953	; PRIOR APPLICATION NUMBER: US/09/969,532 ; PRIOR PLILING DATE: 2001-10-02 ; PRIOR APPLICATION NUMBER: US 60/237,280 ; PRIOR FILING DATE: 2000-10-02
<u>ئ</u> ۾	1954 GOGGITITIGGCIGCAIGICCIGIAACTICCCIGGAITACAACTIGAGAGITITACIGIGIG 2013	Ø
දු පු	2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073 	; TYPE: DNA ; ORGANISM: homo sapiens US-10-798-721-31
8 6	4 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAGGGAATACCTTTAGTCTTCAGATTTCT 	Query Match 68.5%; Score 1873; DB 18; Length 1968; Best Local Similarity 96.3%; Pred. No. 0; Matches 1968; Conservative 0; Mismatches 0; Indels 75; Gaps 2;
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1 & A	94 CGTTCTCCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	QY         754 GATGGGAGCTGGGAAGTGTGGAATGGTCCGTCTGCAGTGTGAACATTTG         813           Db         61 GATGGGAGCTGGGAAGTGTGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG         120
3 6 6	54 CGTTATAGGCCCACTACCACCTGCCTGCAAAATCTGCATTCGGAGCTCAAAAGGC 2	Oy 814 CGGATCCGGGACTGCACACCCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
3 8 8	4 CATGAACAGATCCTCCAAGAGACATCAATCCTAGAGAGTGAAACCATCACATCATAGAGAGAG	Qy 874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAACCTCTTCAT 933
3 & 5	4 ITCTTCGCACAAAGGACACGCACACCCGCACACAGACCAAGAACCAACAA	Qy 934 GAAATAAAACCCCAAAAGCATTGAGAATGCCAGGGACATTGCTTTGTACTCGGGGTTGGGT 993
3 & 5	4 CCCTACTCCATCAGACAGCACTTTCCCTGCACAGACTTGATACCCCCAAAGCCAAGCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGAAG	OY 994 GCTGCCGTCGTGCAGTCCTGGTCATTGGTGTCCCCTTTACAGACGGAGCCAG 1053
සී ඊ සී	S CCCIACICCATCASACAGGGGATITGTGTGCTACATTTGATACCCCCAAATGCCAAAGGCAAG 1  4 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2  5	Qy 1054 AGIGACTAIGGCGIGGACGICAITGACICTICIGCAIIGACAGGIGGCIICCAGACCTIC 1113
8 8 8	59 GACIGGCAGGAIGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 18 54 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 26 55 CAAAGTAGCTCGTTTTTTATAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 26 56 CAAAGTAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	QY 1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
3 8 8	4 GATCTTGACTCCTGCTGTGTTTGAACTGTGGGAAGCTCGTCATCAGCATGATGATGGT 1	Qy 1174 TTTGGTAACTCCCTGGTCCTGCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
g G	1879 GATCTTGACTCCCTGGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACAC	Qy 1234 TACAGCGGACCCATCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293

Db 1546 CATGAACAGATCCTCCAAGTGCAGACATCCTAGAGAGTGAACGAGAAACCATCACT 1605  Qy 2374 TTCTTCGCACAAGAGACAGCACTTTCCCTGCACAGCCCCAAAGCCTTCAAAATT 2433	2554 CAAAGTAGCCCATCTGCTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1786 CAAAGTAGCCCATCTGCTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1786 CAAAGTAGCCCATCTGCTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT	Cy 2614 GATCTIGACTCCTGGCCTTGAAGAGTTGGGGGGGCACACACACACA	2734 TAG 2736 	ESULT 15 S-10-798-721-1 Sequence 1, Application US/10798721	Publication No. US20040248166A1 GENERAL INFORMATION: APPLICANT: Walke, D. Wade APPLICANT: Scoville, John	; TITLE OF INVENTION: NOVEL Human Membrane Proteins and Polynucieotides Encoding the FILE REFERENCE: LEX. 2024-USA ; CURRENT APPLICATION NUMBER: US/10/798,721 ; CURRENT FILING DATE: 2004-03-11		Z O H	; TYYE: DNA ; ORGANISM: homo sapiens US-10-798-721-1	Query Match 59.9%; Score 1640; DB 18; Length 1734; Best Local Similarity 100.0%; Pred. No. 0; Matches 1640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Ay 1 ATGGGGGGGCGCCACCGCAGGGGGGGGGGGGGGGCGCGCTGGCTG	Qy         61 CTGGGGCTGTGCTTCTGGGCGGCGGCGCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120	)  Oy 121 GCCTTCCCGAATCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCA 180	Gy 181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
466 TACAGCGGACCCATCTGCCGAGGACCCTCTGGACAGGACTCATGACAGAGTCCTCA 525 1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCATGGTTTCCCTG 1353 526 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353 1354 GGAGTGTCTGAGAGACTGAAAGTGAAAGTCCAGAGCTCTTTCCCATGGA 1413 586 GGAGTGTCTGAGAGAGCTGAGTACCACGCAAGAATTCCCAGGACTTTTCCCCATGGA 1413 586 GGAGTGTCTGAGAGAGCTGAATACCACGCAAGAATTCCAGGACTTTTCCCCATGGA 645	646 AACAACCACACACTTTACTACTATCCATCCCAGAATAAAATGCCCTACATCCCAAAATCTG 705 1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533 706 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 765	1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593  166 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 825  1594 GAGAATTCTTGGGAGTTTATATATGTCCATCAACCAGGTGAACCCAGCGTCAGAT 1653	826 ĠAĠAATTCTTĠĠĠATTTATAŢĠŢĊĊĀĊĠĀĠĠĀĠĠĠĠĊĊĊĠĠĊĊĠĠĠŢ 1654 ĠGCTCTGAGGTGCTCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713 	1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773	1774 CATITAAAGAAGAGACACAGGGGAAATGGGAGGAAGAGATGATGTCAGTGGAAGATGAA 1833 	1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893 1066 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1125	1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953 	1954 GCGGTTTTTGGCTGCANGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013 	2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073 	CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 21	GICCITGARATTICCCCATTCCTCTGGAGATTAAACCATTCACTGCTGCAGAAGTC 21 GTCCTTGATTTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGC	CCGTTCTCCCCCCTTCCCCTTGGAGABITABACCATTCACTGCCTGCCTGGAGAGACCCCGTTCTTCCCTGGAGAGACCCGGTTCTTCCCTGGAGAGACCGGTTCTTCCCTGGAGAGAGA	CGTTATACGCCCACTACCACCAGCTGCCTGCACTTCGCACTTCGCACTCAGGGC 23 CGTTATACGCCCACTACCACCACCTGCTAAAATCTGCATTCGGCACTCAAAGGC 23 CGTTATACGCCCACTACCACCACCTGCTAAAATCTGCATTCGGCACTCAAAGGC 23 CGTTATATACGCCACTACCACCACACACACACACACACAC	1486 CGTTATACGCCCGCTACCACCCGGGGGGCTGCGGAAATCTGGGTGGG

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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13. (Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Chen, J., Chow, B., Chui, C., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Kam, H.S., Klimowski, L., Jin, Y., Johnson, S., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Sanchez, C., Schoenfeld, J., Varisura, D., Yangura, D., Yil, S., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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BCO48162 Mus muscu
BCO5750 Mus muscu
U87306 Rattus norv
AY97288 Sequence
AA118026 Rattus no
AX497288 Sequence
AX187310 Gallus ga
CQ881060 Sequence
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AX512281 Sequence
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Homo sapiens clone DNA219246 UNC5D (UNQ6012) mRNA, complete cds.
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CQ441583 Sequence
CQ271377 Sequence
CQ721377 Sequence
CQ142137 Sequence
AK122615 Homo sapi
AK122615 Sequence
AK686447 Sequence
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CQ850929 Sequence
AK128132 Homo sapi
AK128132 Homo sapi
AR528525 Sequence
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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1348
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                       /product="UNC5D"
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· 음	AGGGAATGTCACTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGG	임 상	1953 GGACACAGCAGGCAAATGGGAGGAAGTGATGTCAGT 1847 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCT
දු දු	767 AAGTGTGGAGCGAATGGTCCTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAAGT 820 	요 &	2013 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCTCT
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8 %		& A	2087 CAAAATTGCTGCAITTCAAAGGGAATACCTTTAGTCT [
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& g	1307 IGTCGGACATCAAAGIGAAAGICCAGAGCTCGTTCATGGTTTCCCTGGGACTGTCTGAGA 1366 	1 A &	
ð <del>E</del>	1367 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1426 	<b>%</b> 8	
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GCCTTCAAATTCCCTACTCCATCA 2446 CAGCATGATGGTGATCTTGACTCCC 2626 GAAACCATCACTTCTCGCACAAG 2386 2672 2566 2372 TTCTCCCTGGAGCGTTATACGCCCA 2266 2326 2492 2146 2206 1786 2012 CTGGACAGCTTTGGGACCTATGCGC 1906 1966 2132 2026 2192 2252 2312 IGAICGICACCACTCCTTIGCAI 1726 TIGGAAGATGAATCTACATCCTGTT 1846 PAGGIGGACAGCICCTGGAAGAAC 2086 1772 TCCAGTCAGATGGCTCTGAGGTGC 1666 1606 TATTTCGCTACACAAAGTAGCCCAT CTTCAGATTTCTGTCCTTGATATTC TGCCAGGAAGTCCCGTTCTCCCGCG CAGCTCAAAGGCCATGAACAGATCC CAACTGAAGGTGGCGGTTTTTGGCT ||||||||||||||| CAACTGAAGGTGGCGGTTTTTTGGCT STITACTGTGGACAATACCCCTT CCATCCCAGAGGAGTTCTTGGG 3TGGAAGATGAATCTACATCCTGTT ATTGGAATATCCATTTAAAGAAGA

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                                                                     CACTCAGGTGCAAAGCGAGGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGG
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                                                                                                                       CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG
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PAPLINGGAFCEGMSVQKITGTSLCPVOCSWEWSWSPERCEHLLR RECTAPPRN
GGKECEGLSQSEGTOTLDKEPLHEIROSIENASDIALYSGKAAVNAVAUL
IGVTLYRRSQSDYGVDVIDSSALTGGFQTFNFKTVRQGNSLLLNSAMQPDLTVSRTYS
GPICLQPDLDKELMTESSLFPLSDIKTVKVQSSRPANSIVGSRRAETHGGNDLTVSRTYS
ONHGFSTFMPRDRIAFY IQNLSSLFPRELRTTGVFGHLGGRLWPRTOVSLLIPHGA
PERNSRIYMSINGGBPSLQSDGSEVLLSPPENTGCPTPHG
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NTFSLQISYLDI PPPLWR I KPFTACQEVPFGRVWCSNRQPLHCAFSLERYTPTTTQLS
CKICIRQLKGHEQILQVQYSTLLESERETI TFPAQEDSTFPAQTGPKAPKI PYSIRQRI
CATEDTPBNAKGKDWQHAQKNSI INRNLSYFATQSSPSAVILLNIWEARHQHDGDLDSLA
CALEEI GRTHTKLSNI SESQLDEADFNYSRQNGL"
                                                                                                                                                                                                                                                                                                             AB055056 7002 bp mRNA linear PRI 08-JAN-2002 Homo sapiens mRNA for KIAA1777 protein (Unc5h4), complete cds. AB055056
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/db_xref="G1:18150094"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                          TGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAAACTTTCAGAAT
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/codon_start=1
/product="KIAA1777 protein (Unc5h4)"
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/dev_stage="adult"
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iive 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fh19201"
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1007 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGAGGCCAGAGTGACTATGGGG 1066	TGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGAC   TCCGTCAAGGCCAAGAATATCATGGAACTAATGATACAAGAAAA	TRAATTCTGCCATGCCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCA 124	1247 TCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTT 1306 	1307 TGTCGGACATCAAAGTGGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGAAGTGTCTGAGA 1366 1473 TGTCGGACATCAAAGTGAAGTCCAGAGCTCGTCATGGTTTCCCTGGGAGTGTTGAGA 1532 1367 GAGCTGAGAAGAAGAAGAATCCATGCAACCAAGAAACAACAACAACAAGA 1426	GAGCTGAGTACCACGCGAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCAGGCT TAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACCCA TTAGTACAATGCATCCCAGAAATAAAAATGCCCTACATCCAAAATCTGTCATCACCCCAAAATCTGTGTGTTCATCCCCAAAATCTGTGTGTTTTTTTT			1607 AGATTATATGATCCATCAACGAAGGGAACCCAGCTCCAGTCAGATGGCTCTGAGGTGC 1666	1667 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCAT 1726 	1727 TGACCATCCGCACTGTGCAGATGTCAGTTCTGAGCATTGCAATATCCATTTAAAGAAGA 1786 	1787 GGACACAGCAGAATGGCAGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 1846 	1847 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACGACGACCTTTGGGACCTATGCGC 1906 	1907 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 1966 	1967 GCAIGICCIGIAACTCCCTGGAITACAACTIGAGAGITTACTGIGIGGACAATACCCCTT 2026 	GTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAAC	2087 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2146

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2154 CCTCTGGAGAATTAAACCATCACTGCCTGCCAGGAAGTCCCGTTCTCCCGGGTGTGGTG 2213  [	REFERENCE 1 ARBOUTT AX800717 BURARYCKA, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 AUTHORS FITZE TRADING S.A. (CH) ARES TRADING S.A. (CH) ARE

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ARLSDSGNYTCMAAAIVAKRSISATVVVYNVRGWSSWTEWSACNVRCGRGWGKRSRT
CTNRAPLINGGAFFCEGMSVQKITCTALCPVDGSMEVWSEWSVCSPECHLRIRETAPP
PROGRECEGISQESENCYTOCLCILDKELHEIKPOPWSRRGTENASDIALYSGIGAA
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LIVSRYTSGPICLOLDRELMERTSSLEPRIDSDIKVKVQSSFWVSLGVSERASYHGKN
HSGTFPHGNNRGFSTHIPRNKTPYIQNLSSLEPRTELATTGFVFGHLGGBLVMPNYTGN
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HCADVSSEHWILHKRGTQGGKWEFWSVARDSTSCYCLLDPPRACHTLGSFTYALT
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PYSTRQTFCAFGTROLKGEWQMLAGRNSINNLLSYFATGSSPSAVILINLWEARHQQ
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0 CTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAA
10 GAATATCATGGAACTAATGATACAAGAAAATCCTTTGGTAACTCCCTGGTCCTGAATTC 
1200 TGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTG
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1320 AGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGAAGTGTCTGAGAGAGCTGAGTACCA 1373
1380 CGGCAAGAATCATTCCCGATGGAAACAACAACCACAGCTTTAGTACAATGCA 143 
10 TCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACT 
1500 GAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGGCTTAGTAATGCCAATACAGGGT 155 
 1560 GAGCTTACTCATACCACAGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTC 161
1620 CATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGA 167 2054 AATCAACCAAGGTGAACCGAGCCTGCAGTCAGATGGATCTGAGGTTCTCCTGAGTCCTGA 211
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Kits, such as nucleic acid arrays, comprising a majority
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PE Corporation (NY) (US)
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/ Organism="Homo sapiens"
/ Mol type="unassigned DNA"
/ db_xref="taxon:8606"
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	1745 ATGAGGAGACCCTGAACACTGCTACTGCCAGCTGGAGCCCAGGGCTGTCACATCC 1804 1880 TCCTGGACAGCTTTGGGACTATGCGCTCACTGGAGGCCAATCACAGACTGTGAACAGACTGTGAACAGACTGAACAGACTGTGAACAGACTGAACAGACTGAACAGACTGAACAGACTGAACAGACTGAACAGACTATTCCCGCTCAGCAGTCA 1864 1805 TGCTGGACCAGCTGAGCACTACGTGTTCACGGGCGAGTCCTATTCCCGCTCAGCAGTCA 1864	1940 AGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGA 1999	1925 GGGTCTÄCTGCCTGGAGGACCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGA 1984 2060 ATCAAGGTGGACACGCTCCTGGAAGAACCAAATTGCTGCATTTCAAAGGAATACCTTTA 2119 2060 ATCAAGGTGGACGCTCCTGGAAGAACCAAATTGCTGAAGGAATTAAAACCATTACCACA 2044 1985 CTCTGGGGCGATACTTGGTGGAGGAGCCGAAACCGCTAATGCTCAAGGAATTAAAACCATTACCTG 2179		o ccttcrccragagogttatacgcccactaccacctgctcctgcaaaatcrgcattc	2300 GACAGCTCAAGGCCATGAACAGTTCCTCCAAGTGCAGACTCAATCATGAGAAGTGAAC 2359  [	2285 CTGGCTCCCTGGACACTCTGCTGCTGCCCCTGGCAGCTGTCACCCAGCTGGGAC 2344 2417 CCAAAGCCTTCAAAATTCCCTACTCCATCAACAGCGGATTTGTGCTACATTTGATACC 2476 2345 CTTATGCCTTCAAGATCCCACTGTCCATCGCCAAGAAATATGCAACGCCTAGATGCC 2404			25.25 TGCAGCAGGACGACGTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGCCAAGA 2584 2657 CACACACG 2664	2585 GTGAGATG 2592	RESULT 10 25842137 CO842137 2585 bp DNA linear PAT 02-AUG-2004 LOCUS DEFINITION Sequence 784 from Patent EP1440981. ACCESSION CQ842137
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659 AGGCACGGCTCTCGGAATTACACCTGCATGGCACCAACATCGTGGCTAAGA 718 626 AGGCCCGCTGTCGGACACTATACCTGCGTGGCCAAGACATCGTGGCCAAAC 685 719 GGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGCCAAGGCGCAAAC 685 686 GCCGGAGCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAG 769 686 GCCGGAGCACACTGCTCACGTCATGGTCTACGTGAATGGCGGCTGGTCTACGTGGAAG 745	770 TGTGGAGGAATGGTCCGTCTGCAGTCCAGACTGTGAACATTGCGGATCCGGGAGTGCA 829	806 CCAACCCGGTTCTATGGAGGGGCCTTCTGCGAGGGCTTTCCAGAAGACG 865 890 ACTGCACAGATGGTCTTTGCATCCTAGATAAAAACCTCTTCATGAAATAAAACCCCAAA 949 866 CCTGCACCACCATCTGCAACAAAAAAAAAAAAAAA	1010 TIGCAGTCCTGGTCATGGGGGGCTGTTACAGAGGCCAACTGTGTGG 946  1010 TIGCAGTCCTGGTCATTGGTGTCACCCTTTACAGAGGCCAACTGTGTGTG	1064 GCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCA 1120	1067   AGACGCAAGGC	12 12	TCTTTAACCTTTGTCGAACATCTAAAGTCAAAGTTCAAGACTCGTTCATGGTTCCTTTGTCAGGACTCTTATGCTCAGGACTCTTACAGGACTCTTACAGGACTCTTACAGGACTCTTACAGGACTTCTGTGTACAGGTCTACAGCTCCAGGACTCTTTCCCGTTTTCCCCTTACAGGACTTTTCCCCTTACAGGACTTTTCCCCTTACAGGACTTTTCCCCTTACAGAACTCATTCCCCTTACAGGACTTTTCCCCTTACAGAACTCTTTCCCCTTACAGAACTCTTTCCCCCTAGAACTCATTCCCCCTAGAACTCTTTCCCCCTAGAACTCATTTCCCAGAACTCTTTCCCCCTAGAACTCATTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTTCCCCCTAGAACTCATTCCAGAACTCATTTCCCCCCTAGAACTCATTCCAGAACTCATTCCAGAACTCATTCAGAACTCATTCAGAACTCAACAACTCAGAACTCAACAACAACAACAACAACAACAACAACAACAACAA	1265 GGCCAGGCCTGGCAGATGGGGCTGACCTGGTCTTGCCGCCTGGCAATACCCTA 1324  1409 ATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCTACATCCAAA 1468  1325 GCGATTTCGCCCGGGACACTCCTGCACTGCGCAGGCCTCGGTTCCCAGC 1384				1648TCAGATGGCTCTGAGGTGCTCCTGAAGTCACCTGTGGTCCTCCAGACATGA 1705  1565 TTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGACCCACAGGCTCC 1624  1706 TCGTCACCACTCTTGCATTGACCATCCCGCACTGTGCAGTTCTGAGCATT 1765

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Unpublished

1. Chases 1 to 2585)

2. Chases 1 to 2585)

3. Isogal, T. and Yamamoto, J.

Direct Submission

2. Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Exalea-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

ECONOMY, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3'-end one pass sequencing:

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: RAB;

RAB; annotation: HRI and RAB.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, K., Otsuki, T., Sato, H., Kawai-Hio, Y., Saito, K., Nishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Sakine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Sugano, S., Nagahari, K., Masuho, Y., Nagyiyama, A., Kawakami, B., Suzuki, Y., Nugoho, human, CDNA, sequencing project
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Homo sapiens CDNA FLJ16027 fis, clone FCBBF3012170, moderately similar to Mus musculus rostral cerebellar malformation protein (rcm) mRNA.
  943 GCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGT 1002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="cloning vector: pME18SFL3"
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AK122615.1 GI:34527792
oligo capping; fis (full insert sequence)
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/clone="FCBBF3012170"
/tissue_type="brain"
/clone_lib="FCBBF3"
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Pull-Length human cdna
Patent: BP 144091.4 784 28-UUL-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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                                                           Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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CQ842137.1 GI:50893924
                                            Homo sapiens (human)
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Query Match Best Local Similarity 54.3%; Pred. No. 1.4e-153; Matches 1507; Conservative 0; Mismatches 1145; Indels 123; Gaps	Oy 13 GCGGCCACCGCAGGCGGCGGCGCGCCGCCGCTGGCTCCCGTGGCTGGGCTGTGC 72	Qy 73 TICTGGGCGCAGGAACCGCGGCGCCGAGGAACTCACAATGGCGAAGCCCTTCCCGAA 132	Oy 133 TCCATCCATCAGGCCCTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGTT 192  Db 173 TTCCCGTCAGGCCAGCAGCCGCTGCCTACTTCCTGCAGGAGCCAGGACGCCTAC 232	Oy 193 ATTATCAAGAACCTATTGCACTCAGGTGCAAAGGAGGCCAGCCA	Oy 253 TTCAAATGCAACGGCGAGTGCGTCCATCAGAACGAGCACGTCTGGAAGAGTTCTGGAC 312	QY         313         GARGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAG         372           Db         353         GAGGCCACCGGTCTGCGGGTGCCGAGGTGCAGATGGAGGTGTGCGCGCAGCAGGTGGAG         412	Oy 373 GACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGACTCCTCGGGTACC 432	Oy 433 TCCBAGGGAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAACTTTGAACAAGAC 492	QY 493 CCACAAGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCCCCCCACCAGAG 552   1   1   1   1   1   1   1   1   1	OY 553 GGAGTCCCTGCTGCTGGAATGGCTGAAAAATGAAGGCCCATTGACTCTGAACAA 612	0   0   0   0   0   0   0   0   0   0
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Proteins and nucleic acids encoding same
Patent: WO 02057450-A 3 25-JUL-2002;
Curagen Corporation (US).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                    Gaps
                                                                                                                                 123;
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                                                                             Score 592.2; DB 6;
Pred. No. 3.1e-152;
0; Mismatches 1148;
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            db_xref="taxon:9606"
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llarity 54.2%;
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Matches 1504;
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Query Match         21.6%; Score 590.2; DB 6; Length 3933;           Best Local Similarity 54.7%; Pred. No. 1.10-151;           Matches 1562; Conservative 0; Mismatches 1048; Indels 243; Gaps 10;           Qy 13 GGGCCACCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGG		Qy         253 TTCAAATGCAACGGGAGTGGGTCCATCAGAACGAGCACCTCTGAAGAGACTCTGGAC 312           Db         686 TTCAAGTGCAACGGCGAGTGAGCAACGACCACGTCACACAGGAAGCCTTGAAT         745           Qy         313 GAGACTCAGGTTTGAAGGTCCGCGAAGTGTTACTAGCAACAGGTGAG         372           Db         746 GAGGCCACCGGCGTGCGCGAGGTCCAAGTTCCAAGGTGCGCGACGGTGAG         805	Qy         373 GACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGGGGTGCACCTGGGTACC         432           Db         806 GAGCTCTTTGGGCTTGATACTGGTGCCAGTGCCTGGAGCTCCGCGGGCACC         865           Qy         433 TCCAAGAGGAGAGAGACTGTGCGCATAGCCTATTTACGGAAAAAACTTTGAACAAGAC         492           Db         866 ACCAAGAGTCGCCGAGCCTACGCCTACCTGCGCAAGAACTTCGATCAGGAG         925	Qy         493 CCACAAGGAAGGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGG 552           Db         926 CCTCTGGGCAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCGGAG 985           Qy         553 GGAGTCCTGCTGCGGGTGGAATGGCTGAAAAATGAAGACCCATTGACTCTGAACAA 612           Db         986 GGGGTGCTTGGCGGGGTGGAATGGCTGAAAATGAGGGCCATTGACTCTGAACAA 612           Db         986 GGGGTGCTTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCACCCA	Qy         613 GACGAGAACATTGACACCAGGGCTGACCTGATCATCAGGCAGG	1106 GACACTGCAACTGCGGGGGCCAAGACGCCAAACGCCGGGGCCCAT 1165	Qy         768           Db         1286           CTCAACGAGGGCCTTCTGCGAGGGCCAGGCATTCCAGAAGACCCCTGCACCCATC         1345           Qy         768           1346         1611111111111111111111111111111111111
Qy         1993 AACTTGAGAGTTTACTGTGGACAATACCCCTTGTGCATTCAGGAAGTGGTTTCAGAT         2052	Qy         2173 TTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGGGTGTGGTGAGTAACCGGCAGCCCCTG         2232           Db         2333 CTGGCCAAATACCAGAGATCCCCTTCTATCACATTTGAGGTGCCAGAAGGCCCTC         2392           Qy         2233 CACTGTGCCTTCTCCCTGGAGGGTATATACGCCCACTACCACCCAGGTGCTCCTGCAAAATC         2292           Db         2393 CACTGTGCCTTCTCCCTGGAGGGCTATAGGCCCTCCACCAGAGGTCACTGCAAAATC         2452	Qy         2293 TGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCCTAGAG 2352           Db         2453 TGCGTGCGGCAAGTGGAAGGGAGGCCAGATATCCAGCTGCATACCACTCTGGCAGG 2512           Qy         2353 AGTGAACGAAAACGTACACTTTCTTCGCACAAGAGACACTTTCCTGCACAG 2409           Db         2513 ACACCTGCTGGACACTCTCTGCTCTGCTCTGGCAGCACTCTCACCACCCCAG 2572	Qy         2410 ACTGGCCCCAAAGCCTTCAAAATTCCCTACTCAGACAGGGATTTGTGCTACATT 2469           Db         2573 CTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACAGCCTA 2632           Qy         2470 GATACCCCCAATGCCAAAGGCAAGGACTGGCAGAAAAACAGCATCAAC 2529           Db         2633 GATGCCCCAACTGCAATGACTGGCGGATGTTAGCACAGAAAGCTCTTATGGAC 2692	Qy         2530 AGGAATTTATCTTATTTCGCTACAAAGTAGCCCATCTGCTGTTATTGAACCTGTGG 2589           Db         2693 CGGTACCTGAATTACTTTGCCACCAAGGGCCCCAGGGGTGTGATCCTGGACCTCTGG 2752           Qy         2590 GAAGCTCGTCATCAGATGGTGATCTTGACTCCCTGGCCTTTGAAGAGATT 2649           Db         2753 GAAGCTCGCAGGACGATGGAGGACCTCAACAGCGAGGGCTTGAAGAGATT 2812	Oy 2650 GGGAGGACACACG 2664	RESULT 14 CO850929 LOCUS	

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Homo sapiens cDNA FLJ46253 fis, clone TEST14022158, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 (Unc5h2). AK128132
AK128132.1 GI:34535352
oligo capping; fis (full insert sequence). Homo sapiens (human)
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Marsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                     Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai,
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2335 CAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGAC 2391 2924 CATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCTGGC 2983	
2392 AGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAG 2451 	
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2512 CAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCT 2571	
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GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: March 31, 2005, 18:01:54; Search time 8583 Seconds (without alignments) 12133.734 Million cell updates/sec  Title: US-10-798-721-9  Perfect score: 2736 Sequence: 1 atggggagagcggccacgcaggcaaaatggactctag 2736 Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 34239544 seqs, 19032134700 residues Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100%	tist to bummarie ti:*	SUMMARIES Result Query No. Score Match Length DB ID Description	1

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/organism="Pan troglodytes" /mol_type="genomic DNA" /mol_xref="taxon:9598" <1>2507 /locus_tag="HCM0901"	Query Match 68.4%; Score 1871.4; DB 9; Length 2507; Best Local Similarity 83.3%; Pred. No. 0; Matches 2124; Conservative 0; Mismatches 248; Indels 177; Gaps 3;	QY         323 GTTTGAAGGTCCGCGAAGTGTTCATCAAGTTACTAGGCAACAGGTGGAGGACTTCCATG         382	QY         383 GGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGGGCCACCTGGGTACCTCCAAGAGCA         442	Oy 443 GGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAACTTTGAACAAGACCCACAAAGGAA 502	QY         503 GGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGGGAGTCCCTG         562	QY         563 CTGCCGAGGTGGAATGGCTGAAAAATGAAGGCCCATTGACTGTGAACAAGACGAAGA 622	QY         623 TTGACACCAGGCTGACCATAACCTGATCATCAGGCAGGCA	OY 683 ATTACACCTGCAGGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTG 742	Qy 743 TGGTCTACGTGGAAGTGGGAAGTGTGGAAGGGCAATGGTCCGAGTGTCCAGAGT 802 	Qy 803 GTGAACATTTGCGGACTGCACACACACACCACCCCGAGAAATGGGG 853	Qy 854 GCAAATTCTGTGAAGGCCAGGAATCTGAAAACTGCAC	Qy 897 896	Db 601 NINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Db db 120	908 GCATCCTAGATAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCG	Db 721. NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	781 ACMINGETHIGHTHITHITHITHITHITHITHITHITHITHITHITHITHI	Oy 1028 GTGTCACCCTTTACAGAGCGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTG 1087	Qy 1088 CATTGACAGGTGCCTTCCAGACCTTCAACTTCAAACAGTCCGTCAAGAATATCA 1147
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MGSSYSRANVRLQLAI FAPALCTSLEYSLRYYCLEDTPVALKEVLELERTLGGYLVE
PRPLLLFKDS YHNILRUSLHUP PHAHWRSKLLAKYGEI PFYHVWNGSQRALHCTFTLER
HSLASTEFTCKVCKYQVEGEGOI FQLHTTLAETPAGSLDALCSAEGNAI TTQLGFYAR
KI PLISIRQKI CSSLDAPDSRGNDWRLLAQKLSMDRYLNYFATKASFTGVI LDLWEARQ
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LRVREVQIEVSRQQVEELFGLEDYWCQCVAWSSSGTTKSRRAYIRIAYLRKNFDQEPL
AKEVPLDHEVLLQCRPPEGVPVAEVEWLKNEDVIDPAQDTNFLLTIDHNLIIRQARLS
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APLNGGAFCEGQAFQKTACTTVCPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNG
GRDCSGTLLDSKNCTDGLCVLNQRTLNDPKSHPLETSGDVALYAGLVVAVFVVVAVLM
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IYRGPVYALODSADKIPMTNSPLLDPLPSLKIKVYNSSTIGSGSGLAGADLIGVLPP
GIYPGDFSRDTHFLHIRSSALGSQHLIGLPRDPSSSVSGTFGCLGGRLSLPGTGVSLL
VPNGA PQGKFYDL'KHINKARSTLPLEGSGOTVLSPSVTCGPYGLLLCRPVYLTVPH
                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB31108.1"
/db_xref="GI:12857776"
/translation="MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQVLPDSYPSAPA
                                                                                                                                                                                                                     /note="unnamed protein product; TRANSMEMBRANE RECEPTOR
UNC5H2 homolog [Rattus norvegicus] (SPTR|008722, evidence:
FASTY, 96.5%ID, 100%length, match=2835)
                                                                                                /tissue_type="medulla oblongata"
/clone_lib="RIKEN full-length enriched mouse cDNA library'
/dev_grge="adult"
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.larity 54.2%; Pred. No. 8.1e-154;
Conservative 0; Mismatches 1057;
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xref="taxon:10090"
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 532)
CTGTGGGAAGCTCGTCATCAGCATGATGATGTTGACTCCCTGGCCTGTGCCCTTGAA
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Fu.G.K., Wang.J.T., Yang.J., Au-Young,J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone lib="Fib="
/note="Vector: pDrive Cloning Vector"
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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	1645 CAGTCAGATGGCTCTGAGGTGCTCCTGAAG 1681	CD636012/c CD636012		e	/organism="Homo Bapiens" /mol_type="maxh" /db_xref="taxon:9606" /clone llb="Firp" /note="Werfor: Dhrive Cloning Vector"	ORIGIN  Query Match 18.9%; Score 517.4; DB 6; Length 530; Best Local Similarity 99.6%; Pred. No. 6.5e-140;	~ 2_	530 AACTAATGATACAAGAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGC 1211 CAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTG	DD 4.0 CAGAICHGAGCCGGACATACAGCGGACCTAILTGTCGCAGGACCTCTGGGAGATCAGGAGACCTGGGAGATCAGGAGAGAGA	1331 AGAGCTCGTTCATGCTTTCCCTGGGAGTCTTCTGAGAGAGCTGAGTACCACGGCAAGAATC 1350 AGAGCTCGTTCATGGTTT-CCTGGGAGTGTCTGAGAGGCTGAGTACCACGGCAAGAATC	OY 1391 AFTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 1450  DD 291 AFTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 232  OY 1451 AAATGCCCTACAAATCTGTCCACAGCTCACAAGGACAAGAACTG 1510	231 AAATGCCCTACATCCAAAATCAGTCATCACTCCCCACAAGGACAGAACTGAGACAAACTG
Qy         1571 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG         1630           Db         421 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG         480           Qy         1631 GTGAACCCAGCTCCAGTCAGATGGTCTCTGAGGTGCTCCTGAGGTCCTGAAG         161           Db         481 GTGAACCCAGCTCCAGTCAGATGGCTCTCAAGGTGCTCCTGAGGTCCTGAAG         531	6 14/c TION ION N DS	Σ S B S	JOURNAL Genomics 84 (1), 205-210 (2004)  COMMENT Contact: Fu GK  Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102  Email: giudincyte.com.	urce	Query Match Best Local Similarity 93.1%; Pred. No. 2e-143; Matches 593; Conservative 0; Mismatches 1; Indels 43; Gaps 2;	OY 1046 GGAGCCAGAGTGACTATGGCGTGACGTCATTGACTTGAC	QY 1106 AGACCTTCAAAACAGTCCGTCAAGACAAGAATATCATGGAACTAATGATACAAG 1165 Db 535 AGACCTTCAAAACAGTCCGTCAA507	1166 AAAAATCCTTTGGTAACTCCCTGGTCCTGAATTCTGCCATGCAGCCAGATCTGACGGGAGAAGAGAGAG	Dy 1226 GCGGGACATAGGGGGGCCCATCTGCGGGGGCCCCTGGGAGGGCTCATGGAGG 1285  Db 457 GCCGGACATACAGGGGACCCATCTGTGGGGGCCCTCTGGACAAGGGGTCATGACAG 398  OV 1286 AGTCCTCAG-TCTTTAACCCTTTGTCGGACATGAAAGTGAAAGTCCAGAGGTCATCATG 1344	397 AGTCCTCACGTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATG 1345 GTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTT	Db 337 GTTTCCCTGGGAGTGTCTGAGAGGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTT 278  Qy 1405 CCCCATGGAAACAACCACGGTTTAGTACAATGCATCCCAGAAATAAAATGCCTACATC 1464  Db 277 CCCCATGGAAACAACAACTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATC 218	1465 CAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCAT

247 TGTAAAGCAAGCCCTGCCACCCAGATCTATTCAAGTGTAATAGTGAATGGGTTCATCAG 306 283 AACGAGCACGTCTCTGAAGACTCTGGACGAGAGTCTGAAGGGTTCATCAG 306 283 AACGAGCACGTCTCTGAAGACTCTGGACGAGTTGAAGGAAG	463 GCCTATTINOGRAMACTITGANCRAGACCACAGAGACCACTAGACAGAGAGGTCCCTT 487 GCATNANDANDANGCGAAGACATTGACCACAGAGACCCCTAGAGAACGAGTCTCTC 517 GAAGGAATGTTTCTCACTCCCCCCCCCCCCAGAACGAACG
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AY411747 2532 bp DNA linear GSS 12-DEC-2003 Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genemic_survey sequence.
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                                                                                                                                                                                                                                                                                            2602 CAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACAC 2661
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2532)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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2 (Dases 1 to 2532)
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2 (Dases 1 to 2532)
3 (Danowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                  2527 GCTTTCAGCATCCCTCTCCCTATCCGGCAGAAGCTCTGTAGCAGCCTGGATGCCCCAG
GAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAA
                                  2482 GCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCT
                                                                      GCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAAT
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/mol_type="genomic DNA"
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Loure 420, 563-573 (2002)

E (Dases 1 to 3790)

E dachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayachida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakaume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Ta
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GGQLLEBPKALRFKGSIHNIRLSIHDIAHSIWKSKLLAKYQBIPFYHHWSGSQRNLHC
TFLBRLSLMYVELVCKLCVRQVEGEGGIFQLNCTVSEBPTGIDLPLLDPASTITYT
GPSAR'SIPLPIRQKLCSSLDARQTRGHDWRMLAHKLNLDRYLNYFATKSSPTGVILDL
WEAQNFPDGNLSMLAAVLEEMGRHETVVYLAAEGQY"
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ILTLHHCADPSTEDWKIQLKNQAVQGQMEDVVVVGEENFTTPCYIQLDAEACHILTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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unc5 homolog (C. elegans) 3 (MGD|MGI:1095412,
GB|NM_009472, evidence: BLASIN, 99%, match=464)"
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Pred. No. 1.5e-127;
0; Mismatches 1146;
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FaNTOM DB:6030473H24"
/db_xref="taxon:<u>1</u>0090"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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52.6%;
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Best Local Similarity 52.6
Matches 1419; Conservative
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Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

AK031655.1 GI:26327502
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            2585 TGTGGGAAGCTCGTCATCAGCATGATGATCTTGACTCCTGGCCTGTGCCCTTGAAG 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                              2465 CATTIGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAACAGCA
                                                                                                                                                                                                                                                                                                          TCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCCATCTGCTGTCATTTTGAACC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Db 1308 TCTCTACGTGGGGATTGTGATCGCTGTAACAGTCTGTCGCGATCACTGTTGTGGTGGC 1367	Qy 1151AACTAATGATACAAGAAAAATCCTTTGGTAACTCCTGCTCCTGAATTC 1199  Db 1368 CCTGTTTGTGTATCGGAAGAACCACCGTGACTTTGAGTCTGACATCATTGACTCCTCAGC 1427	OY 1200 TGCCATGCAGCCAGATCTGACAGTGAGCGGACATACAGGGACCCATCTGTCTG	Qy 1260 CCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCC 1304	OY 1305 TTGTCGGACATCAAAGTCCAGAGCTCGTTCATGGTTTCCTGGGAGTGTCTGA 1364  DD 1548 TGTCTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGACCACTACCCAACTTGAA 1607	OY 1365 GAGAGCTGAGTACCACGCAAGAATCATTCCAGGACTTTTCCCC 1408	OY 1409 ATGGARACAACCACGTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACAAAA 1468  DD 1668 ATCCAAACTGTCACCCCAGATGACCCAGTCCTTAGAAATGAGGCCCTTAACCTGAA 1727	OY 1469ATCTGTCATCCCCACAAGAACAGAACTGAGGACAACTGGTGTCTTTGGCCA 1523  Db 1728 GAACCAGAGCTCGCAAGACTGACCCATCCTGCACAGCATTTGGTACCTTCAACTC 1787	Qy 1524 TTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACGGTGC 1583  Db 1788 TCTTGGGGGTCACCTCATCATTCCTAATTCAGGAGTAGCTTGCTGGTGGCGC 1847	Qy 1584 CATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAGGGAACCCAG 1640  Db 1848 CATTCCTCAGGGGAGGTCTATGAAATGTGACTGACAGGAAAGAAA	QY 1641 CCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAAGTCACCTGTGGTGCTCCTCAGA 1700	OY 1701 CATGATCGTCACCACTTTGCATTGACCATCCGGACTGTGCAGATGTCTGA 1760  D 1968 AGCTCTGCTGACCCGGCCTGTCACTCTCGCATCACTGTGCAGACCCCAGCACCGA 2027	OY 1761 GCATTGGAATATCCATTTAAAGAAGACACACAGGGCAAATGGGAGGAAGTGATGTC 1820  DD 2028 GGACTGGAAGATCCAGCTCAAAAACCAGGCAGTGCAGGGCACAATGGGAGGATGTTGTGGT 2087	QY 1821 AGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCA 1874	OY 1875 IGIGCICCIGGACAGCITIGGGACCIAIGGGCCCACIGGAGGCCAAICACAGACIGGC 1934	OY 1935 CGTGAAGCAACTGAGCGGTTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAA 1994	Qy 1995 CTTGAGAGTTTACTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGA 2054	QY 2055 AAGGCATCAAGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATAC 2114	2388 CCACAACCTGCGCTGTCTATTCATGACATCGCCCATTCCCTCTGGAAGAGCAAATTGCT
228 CTCCGCCGCTCAAGAAGAAGAAGAAACAAAACAAAACAA	AGCAA           AACAA	207 CCCTATTGCACTCAGGTGCAAAGCGAGGCCATGCAGATATTCTTCAAATGCAACGG 266	267         CGAGTGGGTCCATCAGAACGAGCACCTCTGAAGACTCTGGACGAGAGCTCAGGTTT         3.26	GAAGGTCCGCGAAGTGTTACTAGGCAACAGGTGGAGGTTTCCATGGGC	CGAGGA TATTCCTGCCAGTGTGTGGCTGGAGCCACCTGGGTACCTCCAAGAGCAGGAA	GGCCTCTGTGCGCGTATTTACGGAAAACTTTGAACAAGGCCACAAGGAAGG	507 AGTICCCATIGAAGGCAIGAITGTACIGCACIGCCCCCCCACAGAGGGAGCCCTGCTGC 566			CACCTGCATGGCAGCCAACATGTGGCTAAGAGGAGAGCCTGTCGGCCACTGTTGTGGT	CTACGTGGATGGGAGCTGGGAAGTGTGGAGGAAGGGATGGTCGTCTGCAGTCCAGAGTGTG-	GCGAGGATATAGCGGATCCGGGGGGGGCACCAGCCACCCCCGAGAATGGGAACATTTGCGGATCCGGGGGGGGCACCAGCCACCCCCGAGAATGGG GCGAGGATATAGAAACGCAAAAAACTGCACCAACCCCAGCCCCAGTCAATGGT	ATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCAC	-AGATGGTCTTTGCATCCTAGATAAAAAACCTCT	TCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACT	1128 GAGGGGGGGCCACCACCCCCCAAGAACGGGGGGGAAAGGACTGGGATGGCCTGGTCCT 1187 983 CGGGCTTGGGGCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACA 1042 1188 CCAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	9B	1095 AGGIGGCITCCAGACTICAAAACAGICCGTCAAGAATAICAIGG 1150

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GIGICACCCTITACAGACGGAGCCAGAGTGACTATG - GCGTGGACGTCATTGACTCTTC 1085
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                                                                                                                                                                                                                                                                                                                                                 CCCTATTGCACTCCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGG
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                                                                                   Gape
                                                                                95;
                        Length 2791;
                                                                             Indels
                        Score 475.2; DB 9;
Pred. No. 3e-127;
0; Mismatches 1188;
                              17.4%;
                        Query Match 17.4
Best Local Similarity 52.2
Matches 1403; Conservative
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ANA DNA linear GSS 15-DEC-2003 Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY406493.1 GI:39762467
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                                   CATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAG 2354
                                                                                                                                                                                                                                             2568 TGTGCGGCAGGTTGAAGGAGAGAGAGGCAGATCTTCCAGCTCAACTGTACTGTGTCAGAGGA 2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTCAAACAAGAGGCCATGACTGGAGGATGCTGGCCCATAAACTCAACCTGGACAGGTA 2807
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                                       2628 ACCTACTGGCATCGACTTACCTCTCCTGGACCCTGCTAGTACCATCACCACTGTCACCGG
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Clark, A.G. Glancowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                         CTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCACCAGCTGTCTGCAAAATCTG
                                                                                                                                                     craccrircacreradaadacreadeceraacacagagaacregerrideaaacrera
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CACTGCCTGCCAGGAAGTCCCGGTTCTCCCGCGTGTGCAGTAACCGGCAGCCCCTGCA
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Mus musculus
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'o,D.R., Lu,F., Murphy,B.,
White,T.J., Sninsky,J.J., 1,R., Thomas,P., Kejariwal,A., c.,D.R., Lu,F., Murphy,B., White,T.J., Sninsky,J.J., nomics, 45 West Gude Drive, |||||| GCAGCAGAAGGACAG 2785 ATTTCAGAATCCCAG 2691 03)

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1. 2532	Ouery Match 17.2%; Score 471.8; DB 9; Length 2532; Best Local Similarity 54.0%; Pred. No. 2.9e-126; Matches 1368; Conservative 0; Mismatches 922; Indels 243; Gaps 10;	325 TIGAAGGICCGCGAAGIGITCAICAAGGTAGCCAACAGGIGGAGGACTICCAIGGG 384	385 CCCGAGGACTATTGGTGCCAGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGG 444	445 AAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGG	GAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCT	565 GCCGAGGTGGAAAAGGTGAAGAGCCCATTGACTCTGAACAAGACGAGAACATT 624	625 GACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAAT 684 	TACACCTGCATGGCAGCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTG	1 5	מיני בשינו למשונים למשונים למיני במיני במיני בשינו במינים	481 GGCCGAGGCTGGCAGAAGCGTACTCGGACCTGCACCAGCCCCACTCAATGGAGGC 540	GCCTTCTGTGAGGGACAGGCCTTCCAGAAGACAGCTTGCACCGTGTGCCCAGTGGATTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGG	817 ATCCGGGAGTGCACACCCCCGGGGAAATGGGGGCAAATTCTGTGAAGTCTAAGC 876 817 ATCCGGGAGTGCACACCCCCCGGAAATGGGGGCAAATTCTGTGAAGGTCTAAGC 876 661 ACCCGTAAGTGAAATGAAAATGAAAATGAAGAAATTCTGTGAAAGAAA	CAGGATICTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAACCTCTTCATGAA	ATAMA CCCCA A A GCATTGA GA A TGCCA GCGA CATTGCTTTGTA CTCGGGCTTGGGTGCTTGCTTTGTA CTCGGGA CTTGGTGCTTGGTGCTTGGTGCTTGGTGCTTGGTGGTGCTTGTGTGGTG	GCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGC	841 GCCGICTITGIGGIGGIGGGITCICATGGCCGIGGGGGIGGICGIGIACCGGGGGAAAC 900 1051 CAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAG 1107

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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                      AAACCATTCACTGCCTGCCAGGAAGTCCCGGTTCTCCCGGGTGTGGTGCTAACCGGCAG
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Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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1. 812
/organism="Sus scrofa"
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/db_xref="taxon:9823"
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Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
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/tissue_type="mixed"
//dev stage="from embryos to adults"
//dev stage="from embryos to adults"
//clone_lib="Sus Scrofa library (scan)"
/note="tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, teefis, heart, hypothalamus, pancreas,
miscle, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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Pred. No. 4.2e-117;
0; Mismatches 142; Indels
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/lab host="DH10B"

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CAATCCTAGAGAGAGAACGAGAAACCAT---CACTTTCTTCGCACAAGAGGACAGCACTT 2398
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603214135F1 CSEQRBN13 Gallus gallus cDNA clone ChEST198e9 5', mRNA
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1 (Dases 1 to 896)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Cuprrehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                       GGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCAGCTGT
                                                                                                                  2054 AGAAGGCCCTCCACTCTTCACCCTGGAGAGGCACAGGCTTGGCCTCCACAGAGCTCA
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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/organism="Gallus gallus"
/organism="Gallus"
/moll_type="mRNA"
/strain="Laver"
/db_xref="taxon:9031"
/clone="ChST198e9"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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/dev_stage="adult"
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/done lib="CSEQRBN3"
// note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:

BCORI, Site_2: Not! This normalized library was
CONSTRUCTED from! million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.

Following this first strand synthesis reaction.

Following this first strand reaction, double-stranded CDNA
was blunted, ligated to NotI adapters, digested with
ECONI, size-selected, and cloned into the NotI and ECORI
COMPATIBLE SITES of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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Best Local Similarity 82.0%; Pred. No. 2.8e-101;
Matches 445; Conservative 0; Mismatches 98; Indels 0
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Job time : 8603 secs
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/standard_name= "Single nucleotide polymorphism (SNP)"
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/product= "Novel human protein (NHP)"
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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"Single nucleotide polymorphism (SNP)"

"Single nucleotide polymorphism (SNP)"

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New isolated human proteins and nucleic acids, useful for diagnosing, drug screening, clinical trial monitoring, or treating diseases and disorders, e.g. treating cancer, arthritis, or as antiviral agents.
                                         Claim 1; SEQ ID NO 9; 52pp; English.
2004-591302/57
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Matches 2736; Conserv
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ö 780 540 540 600 999 9 720 The present invention provides novel human proteins (NHP8) and their encoding polynucleotides. The invention is useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders such as cancer and arthritis and cosmetic applications. The invention acts as a cytostatic and virucidal agent. The invention is useful in gene therapy. The present sequence is a novel human protein (NHP) encoding CDNA. The NHP encoding cDNA is located on human chromosome 8. 120 180 180 240 240 300 300 360 360 420 420 480 480 600 120 9 9 GCACGGCTCTCGGGACTCAGGAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA CACCTGGGTACCTCCAAGAGGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC TTTGAACAAAGACCCACAAAGGAAGGTAGGTACCCATTGAAGGCATGATTGTACTGCACTGC GACTCTGAACAAGACGAGAACATTGACACGGGCTGACCATAACCTGATCATCAGGCAG AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGGAAA CTGGGGCTGTTGTTGGGCGGCAGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGGCGTGGAGC caccreseracerecaagascassassecererersesecarasecrarrancesaaaaae TTTGAACAAGACCCACAAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC CGCCCACCAGGGGGGGGTCCCTGCTGCGGGGGGGGAATGGCTGAAAATGAAGAGCCCATT GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC Gaps DB 13; Length 2736; .. 0 Sequence 2736 BP; 713 A; 715 C; 695 G; 613 T; 0 U; 0 Other; Indels . ; Score 2736; D; Pred. No. 0; 0; Mismatches 100.0%; Conservative 421 481 541 601 601 661 721 421 481 541 661

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The present invention provides novel human proteins (NHPB) and their encoding polynucleotides. The invention is useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders such as cancer and arthritis and cosmetic applications. The invention acts as a cytostatic and virucidal agent. The invention is useful in therapy. The present sequence is a novel human protein (NHP) encoding CDNA. The NHP encoding cDNA is located on human chromosome 8.
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cancer; arthritis; cosmetic application; cytostatic; virucidal; gene therapy; human; SNP; single nucleotide polymorphism; chromosome gene; ss.
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iive 0; Mismatches
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96.6%; Score 2642; DB 13; Length 2694;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 42;
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                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 13; 52pp; English
-OCT-2001; 2001US-00969532
                                                  02-OCT-2000; 2000US-0237280P
                                                                                                       (LEXI-) LEXICON GENETICS
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P-PSDB; ADR44591.
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ADR44592 standard; cDNA; 2661

RESULT 5 ADR44592 ID ADR4

3 The present invention provides novel human proteins (NHPs) and their encoding polynucleotides. The invention is useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders such as cancer and arthritis and cosmetic applications. The invention acts as a cytostatic and virucidal agent. The invention is useful in gene therapy. The present sequence is a novel human protein (NHP) encoding CDNA. The NHP encoding cDNA is located on human chromosome 8. 120 GCCCTTCCGGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180 9 8; "Single nucleotide polymorphism (SNP)" /\*tag= d /standard\_name= "Single nucleotide polymorphism (SNP)" CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 1 ATGGGGAGAGCGGCCACCGCAGGGGCGCGGGGGCGCGCCCCCGTGG New isolated human proteins and nucleic acids, useful for diagnosing, drug screening, clinical trial monitoring, or treating diseases and disorders, e.g. treating cancer, arthritis, or as antiviral agents. Novel human protein; NHP; drug screening; clinical trial monitoring; cancer; arthritis; cosmetic application; cytostatic; virucidal; gene therapy; human; SNP; single nucleotide polymorphism; chromosome Gaps "Single nucleotide polymorphism 75; Score 2566; DB 13; Length 2661; Pred. No. 0; 0; Mismatches 0; Indels 75; Sequence 2661 BP; 676 A; 700 C; 688 G; 597 T; 0 U; 0 Other; /\*tag= a /product= "Novel human protein (NHP)" replace(776,C) Novel human protein (NHP) encoding cDNA #8 Disclosure; SEQ ID NO 15; 52pp; English Location/Qualifiers 1. .2661 /\*tag= b /standard\_name= ' replace(788,C) name≕ /standard\_name= replace(1201,T) Query Match 93.8%; Best Local Similarity 97.3%; Matches 2661; Conservative ( 02-OCT-2001; 2001US-00969532 02-OCT-2000; 2000US-0237280P (LEXI-) LEXICON GENETICS INC (first entry) O /\*tag= Scoville J; WPI; 2004-591302/57. P-PSDB; ADR44593. 61 121 g ò

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                                                                            Sequence 7002 BP; 1989 A; 1491 C; 1499 G; 2023 T; 0 U; 0 Other;
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                          В
                         Score 2365.2;
Pred. No. 0;
                                                   0; Mismatches
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llarity 92.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene family, neuron disorder, neuroprotective, gene therapy, gene, human.
                2266 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC
                                                                                                                      GCTACATITIGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC
                                                                                                                                                         AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG
                                                                                                                                                                                                                                                             GAAGAGATTGGGGAGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA
                                                                                                                                                                                                                                                                                2566 GAAGAGATTGGGAGGACACACACAAAACTCTCAAAACATTTCAGAATCCAGCTTGAA
                                                                                                       GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC
                                                                                                                                                                       AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGCTGTCATTTTG
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                                                                 CCTGCACAGACTGGCCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT
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/product= "Novel human neuroprotective protein"
                                                                                                                                                                                                                                                                                                              GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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P-PSDB; AAU98517.
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947 AAAGCATTGAGANTGCOAGCGACATTGTACTTGTACTGGGCTTGGGTGCTGCGTCGTGG 1006 1155 AAAGCATTGAGANTGCCAGCGACATTGTACTTGTACTGGGTGGTGCTGCTGTGCTGTGGTGGTGGTGGTGGTGGT	1667 TCCTGAGTCCTGAAGTCACCTGTGACTCCTCCAGACATGATCGTCACCTCTTGCAT 1726  1833 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCCAGACATGATCCTTTTGCAT 1892  1727 TGACCATCCCGCACTGTGGTCATTCTGAGCATTGAATACCATTTAAAGAAG 1786  1893 TGACCATCCCGCACTGTGGTCAGTTCTGAGCATTGGAATACCATTTAAAGAAG 1952  1787 GGACACAGCAGGACATGTCAGTTCTGAGCATTGGAATACCATTTAAAGAAG 1952  1787 GGACACAGCAGGACAATGGAAGTTCTGAGCATTGGAATCTACATCCTGTT 2012  1847 ACTGCCTTTTGGAATGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 2012  1847 ACTGCCTTTTGGAATGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 2012  1847 ACTGCCTTTTGGAATGGAGGAAGTGATGTCCTGGAAGATGAATCTACATCCTGTT 2012  1953 GGACACAGCCCAATTGCGTGTCATGTGCTCCTGGAAGCTTTGGGACCTATGGCC 2072  1907 TCACTGGAAGACCCAATTGCGTGTCATGTGCTCCTGGAACTGAAGCTTTTGGGCC 2072  1907 TCACTGGAAGACCCAATTACAGACTTACAGACTGAAGCTTTTTTGGCT 2036  1916

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The present invention describes an isolated PRO nucleic acid (I). Also described: (I) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or antibody which specifically binds to a polypeptide of (4); an agonist or composition of matter comprising a polypeptide of (4); an agonist or antibody which specifically binds to a polypeptide of (4); an agonist or comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide or an a sample suspected of having the polypeptide; (11) a method of identifying a compound that inhibits or changing an immune related disease or an inflammatory immune response or an inflammatory immune response or an inflammatory in mammal. The propersion of stimulating the immune response in a mammal. The PRO sequences have antiallargic, antithrandic, immunosuppressive, muscular, had the encoded polypeptides, cempositions, kits and methods of the present sequence or represents a human component of the present sequence represents a human component of the propertion of the present sequence represents a human component of the propertions. The present sequence represents a human component of the propertion or propositions.
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                                                                                                                                                                                                                                            New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTGCCTCATTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG
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28-OCT-2003; 2003WO-US034381
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Db 2553 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGTCTCAAAATTCCCTACTCCATCA 2612  Qy 2447 GACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2506  1	RESULT 8 AD024624 ID AD024624 ID AD024624 AC AD024624; XX	DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7444. XX XW KW ds. XX XX XX XX XX XX NO2004048938-A2.	10-JUN-2004. 26-NOV-2002; 26-NOV-2002; (PROT-) PROT Aziz N, Gin		The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and an anomal soft tissue sample from the same or different individual, determining the expression of agene in both samples and comparing the expression of the soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue carcoma, possibly via gene therapy or vaccine production. The nucleic caid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
		GGACACAGCAGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCC  [	1907 TCACTGAGAGCCAATCACAGACTGTGAAGCAACTGAAGGGGGGGTTTTTGGCT 1966	2087 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2146 2253 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2312 2147 CCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCAGGAAGTCCCTTGTCCCGGG 2206 2113 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCAGGAAGTCCCGTTCTCCCGGG 2206 2313 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGGG 2372	2207 TGTGGTGCAGTAACCGGCAGCCCTGCACTGCCTTCTCCCTGGAGCGTTATACGCCCA 2266  2373 TGTGGTGCAGTAACCGGCAGCCCTGCACTGCCTTCTCCCTGGAGCGTTATACGCCCA 2432  2267 CTACCACCCAGCTGCTCCTGCAAAATCTGCATTCGGCAGCGTTATACGCCCA 2432  2267 CTACCACCCAGCTGCCTGCAAAATCTGCATTCGGCAGCCATGAACAGATCC 2326  2433 CTACCACCCAGCTGCCTGCAAAATCTGCATTCGGAAACAGATCC 2492  2327 TCCAAGTGCAGACATCCTAGAAAGTGAACGAAACCATCATTCTTCGCACAG 2386  2493 TCCAAGTGCAGACATCCTAGAAGTGAACGAAACCATCATTCTTCGCACAG 2552  2493 TCCAAGTGCAGACTCAAACGAGAAACCATCATTCTTCGCACAG 2552  2567 TGCAAGTGCAGAACCAAACCATCATCTTCGCACAAG 2552  257 AGGACAGCACTTCCCTGCACAGACTGACCTCCATCATTTCTTCGCACAG 2552
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The present invention relates to the isolation of human G-protein coupled receptors (GPCRs, designated GCREC), and the polynucleotide sequences encoding them. The GCREC polypeptides or their fragments, and the contouing them. The GCREC polypeptides or their fragments, and the polynucleotides sequences encoding them are useful in diagnosing.

C preventing, and treating disorders associated with an abnormal expression or activity of INTSIG, such as neurodespenarative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. Parkinson's disease), cancers (e.g. leukaemia, cervical or breast cancers), cimmunological disorders (e.g. scleroderma, cervical or breast cancers), cimmunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. acodesseuse), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis). GCREC or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of GCREC. The specifically bind to and modulate the activity of GCREC. The animals to model human disease, ABX17847-ABX1991 represent cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New GCREC polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of GCREC, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and infection.
                                                                                                                                                                                                                                                                                                 , Richardson TW, Swarnakar A, Kallick DA;
Gandhi AR, Lee EA, Elliott VS, Hafalia AJA;
n JA, Baughn MR, Khan FA, Becha S, Lu Y;
y ML, Lal PG, Ramkumar J, Emerling BM, Walsh RT;
Graul RC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 307-308; 313pp; English.
                                                                                                                                                        30-MAR-2001; 2001US-0280683P.
13-APR-2001; 2001US-028314P.
20-APR-2001; 2001US-028736P.
27-APR-2001; 2001US-0287266P.
                                                                                                                  29-MAR-2002; 2002WO-US009923
                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
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Au-Young J, Griffin JA,
Arvizu CP, Borowsky ML,
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                                      WO200279448-A2.
  Homo sapiens
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                     2187 NNNCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCGG
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                                                                            AAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTG
                                                                                                                                                          encoding human G-protein coupled receptor GCREC-63.
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GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG
                                 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG
                                                                            GATTIGIGECTACATTIGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA
                                                                                                                                                                    CATTTTGAACCTGTGGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG
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                                                                                                            GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT
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pregnancy disorder; birth complication; human, gene; ss.
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P-PSDB; ADC77424.
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Transmembrane protein of the neutrin receptor family, and to the use of this protein and the DNA sequence which encodes it for diagnosis, protein and the DNA sequence which encodes it for diagnosis, proteins which are involved in both repelling and attracting axions and the tunction as guidance molecules for cell migration and axon pathing that of the invention have been shown to play a role in diverse physiological functions and they may be involved in many diseases, particularly inflammatory diseases, oncology and cardiovascular disease. Compounds which medulate the transmembrane protein of the invention may therefore have cytostatic, antiinflammatory, immunosuppressive, cardiant, anti-HIV, neuroprotective, notropic, antiparkinsonian, antidepressant, neuroleptic, osteopathic, antiatreriosclerotic, nephrotropic, immunosuppressive, cardiant, the protein and amino acid sequence of the invention may be useful for gene therapy. The protein, nucleic acid (and compound and pharmaceutical composition) of the invention may be useful for the protein and amino acid sequence of the invention may be useful for composition) of the invention may be useful for the medicament for treating disease, such as cell proliferative disorders, medicament disorders, neurological disorders, payeniatric disorders, cardiance developmental disorders, bone disease, atherosclerosis, cardiance and an birth complications. The present sequence is the cloned cannot when the completions. The present sequence is the cloned cannot be cloned the composition of the medicant sequence is the cloned.
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New polypeptide, useful for the manufacture of a medicament for treating disease, e.g., cell proliferative, autoimmune, inflammatory, cardiovascular or neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAAATGAAGAGCCCATTGACTCTGAACAAGAGGAGAACATTGACACCAGGGCTGACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequence which encodes the protein INSP017 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2557; Conservative 0; Mismatches 0; Indels 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2868 BP; 732 A; 748 C; 714 G; 674 T; 0 U; 0 Other;
                                                                                                                                                                                                                        invention relates to a novel human protein (INSP017),
                                                                                                                                                     Claim 9; SEQ ID NO 33; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162
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1554   AGGGGTGAGCTTACTCATACCACCACTCCCACACACACAC
8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
612 GAMANITGARGECCENTEGETCTGARCTCTGARCACTCACCACTCTGACCTCACTCACCACTCACCACTCACCACTCACCACTCACCAC

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The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOV1-NOV44), variants of these proteins, and the polynucleotide sequences encoding them. The NOVX proteins of the invention are G-protein coupled receptor (GPCR) related proteins. The sequences of the invention are useful in the manufacture of a medicament for treating a syndrome related to a human disease associated with the polypeptides e.g. cancer. ABX70402-ABX70499 represent DNAs encoding the human NOVX proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
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                                                                                                                           Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
Guo X, Shanoy SG, Padigaru M, Taupier RJ, Miller CE, Caeman SJ;
Pena CEA, Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;
Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;
Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITCAICAATGITACIAAGGCAACAGGIGGAGGACITCCCAIGGGCCCGAGGACTAITGGTG
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                                                                                                                                                                                                                                                                                                                                                                                      NOVX polypeptides and polynucleotides, useful for treating a syndrom related to a human disease associated with the NOVX polypeptide e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2260; DB 8; Length 2898;
Pred. No. 0;
0; Mismatches 25; Indels 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2898 BP; 750 A; 759 C; 726 G; 663 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 158-159; 413pp; English.
  09-NOV-2001; 2001US-0345399P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.6%;
90.7%;
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Best Local Similarity 90.7
Matches 2562, Conservative
                                                                              (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                WPI; 2003-058423/05.
                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABU52368
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                                                                                                                                 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2868
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                                                                                         ADL24070 standard; cDNA; 2898 BP
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Liu X, Spytek KA, Patturajan M;
Li L, Gorman L, Malyankar UM, Boldog FL;
garu M, Taupier RJ, Miller CE, Casman SJ;
Gusev VY, Smithson G, Zerhusen BD, Gerlach V;
R, Shinkets RA, Rastelli L, Spaderna SK;
Khramtsov NV, Voss EZ, Herrmann JL;
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Vernet CAM, Li L,
enoy SG, Padigaru M,
13-AUG-2001; 2001US-0311978P.
14-AUG-2001; 2001US-0312191P.
16-AUG-2001; 2001US-0312191P.
17-AUG-2001; 2001US-0313626P.
20-AUG-2001; 2001US-0313626P.
27-AUG-2001; 2001US-031562F.
27-AUG-2001; 2001US-031562P.
10-SEP-2001; 2001US-0318403P.
14-SEP-2001; 2001US-0322360P.
14-SEP-2001; 2001US-0322360P.
27-SEP-2001; 2001US-0322360P.
27-SEP-2001; 2001US-0322360P.
09-NOV-2001; 2001US-0332486P.
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defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), tuberous sclerosis, scleroderma, obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, haemophilia, hypercoagulability, idiopathic thrombocytopenia purpura, immunodeficiencies, graft-versus-host disease, AIDS, bronchial asthma, cornon's disease, multiple sclerosis, Albright's hereditary osteodystrophy, diabetes, infectious diseases, anorexia neurodegenerative disorders, latenance's disease, Parkinson's disease, immune disorders, haematopoletic disorders and metabolic disorders. This
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                                                                                                             sequence represents human NOVX cDNA of the invention.
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Human transmembrane protein INSP017 partial predicted gene sequence.
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                                                    GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC
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This invention relates to a novel human protein (INSP017), a transmembrane protein of the netrin receptor family, and to the use of transmembrane protein of the netrin receptor family, and to the use of this protein and the DNA sequence which encodes it for diagnosis.

Chis proteins and treatment of disease. Netrins are a family of secreted proteins which are involved in both repelling and attracting axions and thus function as guidance molecules for cell migration and axon pathchinds processes in the central nervous system. Transmembrane proteins such as that of the invention have been shown to play a role in diverse particularly inflammatory diseases, oncology and cardiovascular disease. Compounds which modulate the transmembrane protein of the invention may therefore have cytostatic, antinflammatory, immunosuppressive, cardiant, anti-HV, neuroprotective, notropic, antiparkinsonian, antidepressant, neuroleptic, osteopathic, antiarteriosclerotic, nephrotropic, immunomodulator, antidiabetic or antiinfertility activity. In addition, the protein and amino acid sequence of the invention may be useful for the manufacture of a composition) of the invention may be useful for the manufacture of a composition) of the invention may be useful for the manufacture of a mediovascular disorders, neurological disorders, psychiatric disorders, cardiovascular disorders, neurological disorders, psychiatric disorders, cardiovascular disorders, hurvinfections, metabolic disorders, pregnancy disorders and birth complications. The protein INSP017 of the invention may be necessed the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the protein INSP017 of the invention may be necessed to the manufacture of the invention may be necessed to the manufacture of
                                          INSP017; transmembrane protein; netrin receptor family; netrin; axion; cell migration; axon path-finding; central nervous system; inflammatory disease; oroclogy; central nervous system; antilflammatory; immunosuppressive; cardiovascular disease; cytostatic; antilflammatory; immunosuppressive; cardiant; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antidepressant; neuroleptic; osteopathic; antiarteriosclerotic; nephrotropic; immunomodulator; antidiabetic; antiarterility; gene therapy; cell proliferative disorder; autoimmune disorder; inflammatory disorder; myeloproliferative disorder; neurological disorder; psychiatric disorder; cardiovascular disorder; neurological disorder; psychiatric disorder; glomerulonephritis; ADS; HIV infection; metabolic disorder; pregnancy disorder; birth complication; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, useful for the manufacture of a medicament for treating disease, e.g., cell proliferative, autoimmune, inflammatory, cardiovascular or neurological disorders.
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/product= "Human INSP017 protein"
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1. .2661
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Sequence 2661 BP; 680 A; 693 C; 670 G; 618 T; 0 U; 0 Other;

the invention.

BP.

DNA; 2661

ADC77421 standard;

RESULT 13

(first entry)

01-JAN-2004

ADC77421;

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  /standard_name= "Single nuclectide polymorphism (SNP)"
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                                                                                                                                                                                                                                     The present invention provides novel human proteins (NHPs) and their encoding polynucleotides. The invention is useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders such as cancer and arthritis and cosmetic applications. The invention acts as a cytostatic and virucidal agent. The invention is useful in gene therapy. The present sequence is a novel human protein (NHP) encoding cDNA. The NHP encoding cDNA is located on human chromosome 8.
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                                                                                                       New isolated human proteins and nucleic acids, useful for diagnosing, drug screening, clinical trial monitoring, or treating diseases and disorders, e.g. treating cancer, arthritis, or as antiviral agents.
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